1199

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TTTATTATCA AGCAATACTT CTCCCTCTAA TGGCTTTATA AGTCGAGACA AGGTTTTAAT      1800

GAGTGTTGAT TTCCCACAAC CATTTGACCC AATAATAACT GATATTTTTT CTTCAGGTAT      1860

TTTTATATTT ATATTTTCCA AGATTATTTT TTCATCATAA CCGCAGGTAA GATTATTTGA      1920

CCACAGACCT TTCATTATAT ATTCCTCCTG TTCATTTTTA TTAGTAAGTA TATTAAGTAT      1980

GGTGAACCTA ACAAGCCAGT TACAACACCT ACTGGATATC TAGCTGGTAA AATATTTTGA      2040

GAGAATATGT CTGATAACAA AACTAGTAAA ATTCCAACCA ATCCAGCTAA TATTGGGCTT      2100

CTTTTCTTGC CAATATTTAA GGCTATGGGA CCAGCTAAAA AAGATATACA AGCTATTGGT      2160

CCTGTAATTG AAGTAGAAAA AGCAGTTAAA GATACAGCGC AAAAAATTAA AACAAGCCTT      2220

GAAAGCTCGG GATTTGCTCC AAGTCCGATT GCTATTTCTT CACCAAGTTC AATAATTTCT      2280

AGTCTTTTAT TAAAAAATAA AACTAATATA GTAGCAATAA TACTTACTAT TAGAACAAGA      2340

GGTATGTCAT CTAACTTTGT AAAAGATAAA GAGCCACTGA GCCATCTCAT AACTTCTTGT      2400

AATTCATATC TTGCTACTTT CAACAATAAA AATGAGGTGC CTGCTCTTGT GACAGCTTGA      2460

AAACCAATAC CTAATATTAT CAGTCTTGCT GCTGAAAAAC CATCTTTTTT AGCTAGTAAA      2520

AATAATATTA AAGATGATGT TAGTCCACAA GTTATTGAAA TAATTCCAGT AGTTAAACTA      2580

TTTGTTTTTA ATACCAATAT GCAAAAGACC GCTGCAATAG ATGAAGAACT TGTGACACCG      2640

ATTATATCAG GACTTGCAAG AGGATTTCTT AACATAGTTT GAAAGATAAA TCCTGCCAAT      2700

CCAAAAGACC AGCCAGCTAT AATTCCTGCT AATAATTTTG GTAATCTAAT TTCCATAATC      2760

GAAAAACTAG CTCCAGGAAC AGTTTCACTA TTTAAGACTT TAATCAAAGT TGAAAAAGAA      2820

TAACTTTCAT CTCCGATAAG TAAAATGAAA AATGATAGAC TGATTATTAT TAATAAAAAT      2880

AGTGAGGAAA ATAGTGTTAT TCTATTTTTT CTTTTTTGAA TACCTATAAT TAAATTTTGC      2940

ATTAGTTATT AACCCCTCTA TTTTTCATAG TTACATAAAT AAGTACTGGA CCCCCGATTA      3000

TTGCAGTAAT TATCCCTACT TCAATTTCAC CTGGTTTACC TAACATACGG CCGATTATAT      3060

CACATATAAG CAAGAGCTCT GCACCTATAA AAGATGAAGA AATGGTCATT GTGCGTATAT      3120

CTTTGCTTAT AAATAAGCCA CAAAAGTGAG GAACTATAAG ACCTACGAAG CCAATAGGTC      3180

CACCAATTGC AGTAATACTT GAACATAAAA GCACACTTGC AATTATTGCA AGTGATCTTA      3240

TCCTATTAAC ATTAACTCCA AGACCAACAG CCATTTCATC ACCCATAGcT AAAGCGTTTA      3300

AATCTGATGA AATAAATATA GCTATCAAGT GACCTAAAAT TATAAAAGGT AGTAGTGTAG      3360

ATATAGAAGA TAATGTAGCT GCTCCAAGGC TACCTATTTG CCAAAATCTA AATTTGTCTA      3420

AGACGTTATT ATTCGGTAAA ATTAAAAAAC TTACAAAACT GCTTAAAGCC ATACTAACAC      3480
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                                            1200
AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCCTGC TTTTCCGTTA CAGCAATCGC   3540

GTATACAAAA ATTGCACTTA CTAAGCCACC AATGATTGCG   3580

(2) INFORMATION FOR SEQ ID NO: 210:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 11378 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAATTAT TATGGAGTCG TCGTTTGGCA GATGGGCGTG ATATGTGTGC   60

TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAATCGT   120

CAATATTTTA ACCCGTCTTC ATCGCTCACG TCCGTTGATG ACACAATTGA GTCGTTTGGG   180

CTATGCCATG GAAACACCTG TAGATTTACT ACAGTCTTGG CAGGAAACGG CTCCAGATGC   240

TTTGCGTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTCAGA CTATTCCAGG   300

ATTTAGAGAG GACCATGCGA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGGATTGA   360

GACAGATAGT GGCTTGATTT ATTTAGTAGA TTGGGATTCG GTTCGCTTGA CCGATCGCAT   420

GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTCAGAA CATCAGTGGA AGGAATGGTT   480

GACCTACTAC GGTTACAAGT ACAATCAAAC GGTATTAAGT AAATTGTATT GGTATGGTCA   540

ATTGTCTTAT TTGAGTCAGA TTTCCAAGTA TTATATGAAC CAAGATTTAG AAAATGTCAA   600

TCGGGAGATT CATGGTTTGC GTCATTTCCG AGACAAGTAT GGAAAGAGAA GATGAGAGTT   660

AGAAATCGTA AAGGGCAAC AGAATTACTA GAGGCAAATC CCCAGTATGT GGTCCTCAAT   720

CCCTTGGAAG CCAAGGCAAA ATGGCGGGAC TTGTTTGGCA ATGATAATCC CATTCATGTG   780

GAAGTTGGAA GTGGAAAGGG TGCCTTTGTT TCAGGTATGG CCAAGCAAAA CCCTGACATC   840

AACTATATCG GGATTGATAT TCAAAAGTCT GTTTTGAGCT ACGCTTTGGA CAAGGTGCTT   900

GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGGTAGATG GTTCTGACTT AACTGACTAC   960

TTTGAAGACG GTGAGATTGA TCGCTTGTAT CTGAACTTTT CAGATCCATG GCCGAAAAAA   1020

CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCTTCTTGG ATACCTTCAA ACGTATCTTG   1080

CCTGAAAATG GAGAAATTCA TTTCAAGACG GATAACCGTG GCTTGTTTGA GTACAGTTTA   1140

GTGAGCTTTT CTCAATATGG CATGAAACTC AATGGTGTCT GGTTAGATTT GCATGCCAGT   1200

GATTTTGAAG GCAATGTCAT GACAGAATAC GAGCAAAAAT TCTCAAACAA GGGGCAAGTT   1260

ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGCTT   1320

1201

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TTGCTTTACA TAAGTTGGCA AACGTGCTAT ACTGATAGTA AGAATATGAA AAGTGAGGCG     1380

GGGAAATATC TTCGCCTCTT GCTTATGAGG AGGTGGACGC AATCGCAACA ATCGTAGAAT     1440

TAGTCAGAGA AGTTGTAGAA CCTGTCATAG AAGCTCCTTT TGAACTCGTG GATATCGAGT     1500

ATGGAAAGAT TGGCAGTGAC ATGATTCTCA GTATTTTTGT AGATAAACCC GAAGAATTAC     1560

CTTGAACGAC ACGGCAGACT TGACAGAAAT TATCAGTCCT GTCCTAGACA CCATCAAGCC     1620

AGATCCCTTC CCAGAACAAT ATTTCCTAGA AATTACCAGT CCAGGTTTGG AACGTCCTTT     1680

GAAAACCAAG GATGCCGTCG CTGGAGCGGT TGGAAAATAC ATCCATGTCG GGCTCTACCA     1740

AGCCATCGAT AAGCAAAAGG TCTTTGAAGG AACCTTGTTG GCCTTCGAAG AGGACGAGTT     1800

GACTATGGAA TATATGGACA AGACGCGTAA GAAAACCGTC CAAATTCCAT ACAGTTTAGT     1860

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AAAGTGAAGA AAACATGAGT AAAGAAATGC TAGAGGCCTT CCGCATTTTG GAAGAAGACA     1980

AGGGAATCAA AAAAGAAGAT ATCATCGACG CAGTAGTAGA GTCGCTTCGT TCCGCTTATC     2040

GCAGACGCTA TGGTCAGTCA GACAGCGTAG CTATTGACTT CAACGAAAAA ACAGGTGACT     2100

TTACAGTTTA TACTGTCCGT GAAGTTGTTG ATGAAGTATT TGATAGCCGT TTGGAAATCA     2160

GCTTGAAAGA TGCTCTTGCC ATTAATTCAG CTTATGAACT TGGAGACAAA ATCAAGTTTG     2220

AAGAAGCACC AGCTGAGTTT GGTCGTGTAG CAGCCCAATC TGCCAAACAA ACCATCATGG     2280

AAAAAATGCG CAAgCAAACA CGTGCCATCA CTTACAATAC TTACAAAGAA CATGAGCAAG     2340

AAATCATGTC TGGTACAGTA GAACGCTTTG ACAACCGCTT TATCTATGTC AACCTTGGTA     2400

GCATCGAAGC CCAATTGTCA AAACAAGACC AAATTCCTGG AGAAGTTTTT GCTTCTCATG     2460

ATCGTATCGA AGTTTATGTT TACAAGGTTG AAGACAACCC TCGTGGTGTG AACGTCTTTG     2520

TTAGCCGTAG TCATCCAGAA ATGATCAAAC GTTTAATGGA GCAAGAAATT CCAGAAGTTT     2580

ATGATGGAAC TGTTGAAATC ATGAGCGTGG CTCGTGAAGC AGGTGACCGT ACGAAGGTTG     2640

CTGTTCGTAG CCACAATCCA AACGTGGATG CTATCGGTAC AATCGTTGGA CGTGGTGGTG     2700

CTAATATCAA GAAGATTACT AGCAAATTCC ACCCAGCTCG TTACGATGCT AAAAATGACC     2760

GCATGGTACC AATCGAAGAA AATATCGATG TTATCGAGTG GGTAGCAGAT CCAGCTGAAT     2820

TTATCTACAA TGCCATCGCT CCTGCTGAGG TTGACCAAGT TATCTTTGAT GAAAACGACA     2880

GCAAACGTGC CTTGGTGGTT GTTCCAGATA ACAAGCTTTC TCTTGCCATT GGTCGTCGTG     2940

GACAAAACGT GCGCTTGGCG GCTCACTTGA CTGGTTACCG TATCGATATC AAGTCTGCTA     3000

GCGAATTTGA AGCCATGGAA GACGCTGCTT CAGTAGAGTT GGAAGTAGAA AACGATACTG     3060
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1202

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TAGAAGAATA AAAGCTGCTA GAGGAGGGAA AGATGAAAAC AAGAAAAATC CCTTTGCGCA    3120

AGTCTGTTGT GTCTAACGAA GTGATTGATA AGCGTGATTT GCTCCGCATT GTCAAGAACA    3180

AGGAAGGACA AGTCTTTATT GATcCTACGG GCAAGGCCAA TGGCCGCGGC GCTTATATCA    3240

AACTAGACAA TGCAGAAGCC CTAGAGGCGA AAAAGAAGAA GGTCTTTAAC CGCAGCTTTA    3300

GCATGGAAGT GGAAGAAAGC TTTTATGACG AGTTGATCGC TTATGTGGAT CACAAAGTGA    3360

AAAGAAGAGA GTTGGGACTT GAATAAGCAA AAGATAAGTA ATCTCTTGGG GCTTGCTCAG    3420

CGAGCAGGGC GCATCATATC GGGTGAAGAA TTGGTGGTCA AGGCCATTCA AGACGGCAAG    3480

GCCAAGTTGG TCTTTCTAGC TCATGATGCT GGACCCAATC TGACCAAGAA GATTCAAGAT    3540

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GCAGTCGGGA AATCGAGAAA GGTTTTGGCT GTAACAGATG CTGGATTTAC AAAGAAAATG    3660

AGGTCTCTTA TGGAATAGAA GAGGAGGACA TGATTTGTCT AAGAAAGAT TGTACGAAAT    3720

CGCAAAAGAA CTTGGAAAAG AAAGTAAAGA AGTTGTAGCG CGTGCAAAAG AGTTGGGCTT    3780

GGATGTGAAA AGCCACTCAT CAAGTGTGGA AGAAGCTGTC GCTGCAAAAA TTGCTGCCAG    3840

CTTTAAGCCT GCAGCTGCTC CGAAAGTAGA AGCAAAACCT GCAGCCCCAA AAGTAAGTGC    3900

AGAAAAGAAA GCCGAAAAAT CTGAGCCAGC TAAACCAGCT GTAGCTAAGG AAGAGGCAAA    3960

ACCTGCAGCC CCAAAAGCAA GTGCAGAAAA GAAAGCCGAA AAGTCTGAAC CAGTAAAACC    4020

AGCTGTAGCC AAGGAAGAGG CAAAACCAGC TGAGCCAGTC ACTCCGAAAA CAGAAAAAGT    4080

AGCGGCTAAA CCGCAAAGTC GTAATTTCAA GGCTGAGCGT GAAGCACGTG CTAAAGAGCA    4140

GGCAGAGCGA CGCAAGCAAA ATAAGGGCAA TAACCGTGAC CAACAACAAA ACGGAAACCG    4200

TCAGAAAAAC GACGGCCGTA ATGGTGGAAA ACAAGGTCAA AGCAACCGCG ACAATCGTCG    4260

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GCAAGAGGAT AAACGTTCAA ATCAAGCGGC TCCACGTATT GACTTTAAAG CCCGTGCAGC    4380

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CTTTGAAGAA GCGGCTAAGT TAGCTGAACA AGCACAGCAA GTTCAAGCAG TGGTTGAAGT    4560

CGTCCCTGAG AAAAAAGAAC CTGCAGTGGA TACACGTCGT AAAAAACAAG CTCGACCAGA    4620

CAAAAATCGT GACGATTATG ATCATGAAGA AGATGGTCCT AGAAACAAC AAAAGAATCG    4680

AAGTAGTCAA AATCAAGTGA GAAATCAAAA GAATAGTAAC TGGAATAACA ACAAAAAGAA    4740

CAAAAAAGGC AATAACAAGA ACAACCGTAA TCAGACTCCA AAACCTGTTA CGGAGCGTAA    4800

ATTCCATGAA TTGCCAACAG AATTTGAATA TACAGATGGT ATGACCGTTG CGGAAATCGC    4860
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1203

AAAACGTATC AAACGTGAAC CAGCTGAAAT TGTTAAGAAA CTTTTCATGA TGGGTGTCAT   4920

GGCCACACAA AACCAATCCT TGGATGGGGA AACAATTGAA CTCCTCATGG TGGATTACGG   4980

TATCGAAGCC AAACAAAAGG TTGAAGTGGA TAATGCTGAC ATCGAACGTT TCTTTGTCGA   5040

AGATGGTTAT CTCAATGAAG ATGAATTGGT TGAGCGTCCA CCAGTTGTTA CTATCATGGG   5100

ACACGTTGAC CACGGTAAAA CAACCCTTTT GGATACTCTT CGTAACTCAC GTGTTGCGAC   5160

AGGTGAAGCA GGTGGTATTA CTCAGCATAT CGGTGCCTAC CAAATCGTGG AAAATGGTAA   5220

GAAGATTACC TTCCTTGATA CACCAGGACA CGCGGCCTTT ACATCAATGC GTGCGCGTGG   5280

TGCTTCTGTT ACCGATATTA CGATCTTGGT CGTAGCGGCA GATGACGGGG TTATGCCTCA   5340

GACTATTGAA GCCATCAACC ACTCAAAAGC AGCTAACGTT CCAATCATCG TAGCTATTAA   5400

CAAGATTGAT AAACCAGGTG CTAACCCAGA ACGCGTTATC GGTGAATTGG CAGAGCATGG   5460

TGTGATGTCA ACTGCTTGGG GTGGAGATTC TGAATTTGTT GAAATTTCGG CTAAATTCAA   .5520

CCAAAATATC GAAGAATTGT TGGAAACAGT CCTTCTTGTG GCTGAAATCC AAGAACTCAA   5580

AGCAGACCCA ACAGTTCGTG CGATCGGTAC GGTTATCGAA GCGCGCTTGG ATAAAGGAAA   5640

AGGTGCGGTC GCAACCCTTC TTGTACAACA AGGTACCTTG AATGTTCAAG ACCCAATCGT   5700

TGTCGGAAAT ACcTTCGGTC GTGTCCGTGC TATGACCAAC GACCTTGGTC GTCGTGTTAA   5760

AGTTGCTGGA CCATCAACAC CAGTCTCTAT CACAGGTTTG AACGAAGCAC CGATGGCGGG   5820

TGACCACTTT GCCGTTTACG AGGATGAAAA ATCTGCGCGT GCAGCAGGTG AAGAGCGTGC   5880

CAAACGTGCC CTCATGAAAC AACGTCAAGC TACCCAACGT GTTAGCCTTG AAAACCTCTT   5940

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GACTATCGTC CACTCAGCGG TCGGTGCTAT CAACGAATCA GACGTGACCC TTGCCGAAGC   6120

TTCAAATGCC TTTATCGTTG GTTTCAACGT ACGCCCTACA CCACAAGCTC GTCAACAAGC   6180

AGAAGCTGAC GATGTGGAAA TCCGTCTTCA CAGCATTATC TACAAGGTTA TCGAAGAGAT   6240

GGAAGAAGCT ATGAAAGGGA TGCTTGATCC AGAATTTGAA GAAAAAGTTA TTGGTGAAGC   6300

GGTTATCCGT GAAACCTTCA AGGTGTCTAA AGTGGGAACT ATCGGTGGAT TTATGGTTAT   6360

CAACGGTAAG GTTGCCCGTG ACTCTAAAGT CCGTGTTATC CGTGATGGTG TCGTTATCTA   6420

TGATGGTGAA CTCGCAAGCT TGAAACACTA TAAAGACGAC GTGAAAGAAG TGACAAACGG   6480

TCGTGAAGGT GGATTGATGA TCGACGGCTA CAATGATATT AAGATGGATG ATGTGATTGA   6540

GGCGTATGTC ATGGAAGAAA TCAAGAGATA AGATTTTTTG CTCCTTTCTT AGGTGGTGAG   6600

1204

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GGACGCAAGC AAACCGATGG TTTCATTGCT TATTTTTGAG CCTAGGGTCT CAAAAATCCC        6660

CTGTGATGGG ACTGATAAAT CAGTTCCATC ACTTTCACCA CGGCGAAAGA AGCAGATGAC        6720

TTCAAATTGA ACTTCGTTTC AATTTAAACT GAAAATCAAG AAGTTTAAAA TAGCTAGGTC        6780

TGCTGGCCTA GCTTTTGGTT CAAAGTAGAG AAAGGAATAT CATGGCAAAT CATTTCCGTA        6840

CAGATCGTGT GGGCATGGAA ATCAAGCGTG AAGTCAATGA GATTTTGCAA AAGAAAGTCC        6900

GTGATCCACG TGTCCAAGGT GTGACCATCA TAGATGTTCA GATGCTGGGT GACTTGTCTG        6960

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TCGGGCTTGA AAAAGCAACT GGTACCATCA AACGTGAACT TGGTCGCAAT TTGAAATTGT        7080

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TGTCCTGTTC TTGTTTCATT TTAATATAAA AAAGGGATTC TGTATTTTTT AATGTTATCT        7380

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TCAATTTTAT GCTTTCTCTC TGAAATTGGC TCAAGAATTA GGTTATATTT ATGGTTATGA        7800

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CCGTGCAAGG TGTAAAAGTG ATGAAAACGA TAAAGAAAGC TGACCATGTC GTTGTTGGTC        8340

TGGGGAAACT TTTTATTGCC GACAAGTTAA TGGATACGGC TCGGTGGCTC ATTAAGCCAG        8400
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1205

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AGGAGAGAGA ATGAAATTTT TTTGGTCTTC TTGCTATTCT TTTTATCAAA CCGATTATTG    8460

GGATTGTGAA ATTCTTTTGG ATGATCATCT CTTTTGCAGT CCAATTGCTG TTTTACAAGA    8520

TAGTGTTTAA GATATTGGAT TGGCTCTTTA AACTTATCTA GATGGTAATC CAAGTTGCAG    8580

AGAACTAGCA GGAACTCCAC TGCTAGTTTT TTATTCTCTT TCCATATGGT ATAATATAAG    8640

CAGTAAAATC ATTTTATACT CTTCGAAAAT CTCTTCAAAC CACGTCAGCT TCACCTTGCA    8700

GTATATATGT TACTGACTTC GTCAGTTCTA TCCACAACCT CAAAACGGTG TTTTGAGCTG    8760

ACTTCGTCAG TTCTATCTAC AACCTCAAAA CACTGTTTTG AGCAACCTGC GGCTAGCTTC    8820

CTAGTTTGCT CTTTGATTTT CATTGAGTAT TAGAACATAC AATGGAGGTC GTCATGGACA    8880

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AAATTCTAGT GGAGTTGGGT TTTAAACCCC TTGCCAATCC CTTAATGCGC AATACAGTTG    9000

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CATCCGTCCG TCAGAGAAAT GGGTGCCAGA ACGACAGAGC TTTATTGAGG AAAAGATTGC    9900

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TCATCTCCCT ATGGAGATTA CCTTTGTCAA TAAAGAAGAT ATTTTCCAGT ATTACAATGA    10140
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1206

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CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GGCGCAATGT    10200

CGAACTCTGC CATCCGCCTA AGTACTTGGA CAAGGTCAAA ACTATCATGA AGGGGCTTCG    10260

TGAGGGAAGC AAAGACAAGT ATGAAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT    10320

CCACATCACC TATGCTGCAG TACACGATGA AGACGGAGAA TTCCAAGGAG TGTTGGAGTA    10380

TGTTCAGGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA    10440

AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTTGAAGCTT GGGTCAATAC    10500

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TTCAAAAACT GGACTGAAAA AGAACTCCTT GCCTTGAAAG GAATCGGCCC AGCTACCATC    11160

AAGAAATTGA AAGAAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCATTTCCG    11220

AAAAAATCTT GCTACAATAG AGCCATTAGA GGTGTTTTGA ATCCCACATT TTACAGAAAG    11280

TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAAACTGGTT GCTAATGGAT GAAAAATTGA    11340

AATAAAAGTG TCTTTTTGCT TTAAAGACGA GAGTTGCG                            11378
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(2) INFORMATION FOR SEQ ID NO: 211:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4156 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

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CCGCGAGCCA CGGCGAATTT GCTGCGGGTA TTCATCAGTC AGGATCTATG ATCTTTGGTG    60

AACAAGAAAA GGTTCAAGTT GTGACCTTTA TGCCAAATGA AGGTCCTGAT GATCTATACG    120

CTAAGTTTAA TAACGCTGTT GCTGCATTTG ACGCAGAAGA TGAGGTTCTA GTTTTGGCTG    180
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1207

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ACCTTTGGAG TGGTTCTCCA TTTAACCAAG CTAGTCGCGT GATGGGAGAA AATCCTGAGC    240

GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC    300

GCCTCATGGA CGCTGCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA    360

AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG    420

CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTTATCGGA GACGGTAAAT    480

TGAAAATCAA TCTTGCCCGT CTTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT    540

GGACTCCAGA TTCAAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTG GCTAAAGACG    600

ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCCAGGTAA TGTCAAGGCT AACGTGGTTC    660

CAATTCAAAA ACTGATTGAG ATTTCAAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA    720

TCTTGTTTGA AACACCTCAA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA    780

CTCTTAATGT TGGTTCTATG GCTCACTCAA CAGGTAAAAC ATTGGTCAAT ACCGTTTTGT    840

CTATGGACAA AGAAGACGTT GCTACATTTG AAAAAATGCG TGACTTGGGT GTTGAATTTG    900

ATGTCCGTAA AGTACCAAAT GATTCTAAAA AAGATTTGTT TGACTTGATT AACAAAGCCA    960

ATGTCAAATA AGCCATTATT TATGAAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT   1020

TAGTAGTCGT TGTAGCCTTC TTTGCAGGTC TTGAAGGCAT CCTCGACCAG TTCCAATTTC   1080

ACCAACCACT TGTAGCCTGT ACCCTTATTG GGCTTGTAAC AGGTCACTTG GAAGCAGGGA   1140

TTATCCTCGG TGGATCGCTT CAAATGATTG CCCTTGGTTG GTCAAATATC GGTGCTGCTA   1200

TCGCTCCTGA TGCTGCACTT GCTTCTGTCG CTGCTGCCAT TATCATGGTT CTTGGTGGTG   1260

ACTTTACCAA GACTGGTATC GGTGTTGCCC AAGCGGTTGC TATCCCTCTT GCTGTAGCTG   1320

GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAGTTGG TTTGGTTCAT ACTGCAGATG   1380

CTGCCGCTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTCATC GCGCTACTTT   1440

TCCAAGGACT TCGTATCGCG CTTCCTGCAG CTCTTCTCCT TATGGTACCA ACTGAAACTG   1500

TACAAAGTAT CCTTAGTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGGTGGTG   1560

GTATGGTCGT TGCCGTTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT   1620

GGCCATTCTT CGCTCTTGGT TTCGTTCTCG CTGCTGTGTC AGATATTACT CTAATCGGAT   1680

TCGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTTCTAAA ACTGGTGGAA   1740

ATGGTGGCGG AGGAGCCGCA ACTTCTAACG ACCCAATCGG CGATATCCTA GAAGACTACT   1800

AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAAACTT CAATTAACTA AATCAGATCG   1860

TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGGTCT TGGAACTTTG AACGGATGCA   1920
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1208

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AAACTTGGGC TGGGCTTATA CACTCATTCC AGCTATCAAA AAACTCTATA CTAAAAAAGA    1980

AGATCAAATC GCTGCTCTTG AGCGTCACCT TGAGTTCTTC AACACTCATC CATACGTAGC    2040

TGCTCCAGTC ATGGGGGTTA CTCTTGCGCT TGAAGAAGAA CGTGCTAACG GTGTGGAAAT    2100

CGATGACGCT GCTATCCAAG GGGTTAAAAT CGGTATGATG GGACCTCTTG CTGGTATCGG    2160

TGACCCAGTA TTCTGGTTTA CAGTACGCCC AATCCTTGGA TCTCTCGGTG CTTCACTTGC    2220

CCTTACTGGC AATATCTTGG GGCCACTCCT CTTCTTTGTT GCATGGAACT TGATTCGTAT    2280

GTCATTCTTG TGGTATGTTC AAGAGATTGG ATACAAGGCT GGATCAGAAA TCACTAAAGA    2340

TATGTCTGGT GGTATCCTTC AAGATATCAC TAAAGGAGCT TCTATCCTTG GGATGTTCAT    2400

TCTTGCTGTC CTTGTTCAAC GCTGGGTAAA TATTAAATTT GCTTTCGATG TTTCTAAAGT    2460

TCAACTAGAT GAAAAGGCTT ATATCCATTG GGATAAATTG CCAGAAGGGT CTAAAGGTAT    2520

CCAAGAAGCA TTCGCACAAG TAGGACAAGG ATTGTCTCAA ACTCCTGAAA AAGTTACTAC    2580

TTTCCAACAA AACTTGGATA TGTTGATTCC TGGATTATCA GGACTACTCC TTACTTTACT    2640

TTGCATGTAC TTACTTAAGA AAAAGTATC TCCAATCACT ATTATCCTTG CCCTCTTCGC    2700

AGTGGGTATT GTGGCACATG TTCTTCACAT CATGTAATCA AGCAACTAAA AAGGAACCAG    2760

GTTCTAAAAT CTGATTCCTT TTTTCTATGC TTTTATTCAG CCAAGGCTCC CATTGGATCC    2820

CATGGTGCAA GTACGATTGG TTCTGCTCCA TAGGCAGCTT GTTCTTCTGC TGTCAGCAAT    2880

TCCTTACGAA CAACGATTTG GTATGTGTAT TCGTCCATCC AAGCGTCTGA GGCAACAAAG    2940

TAACCATCTG TACCGACCTT GTCTCCCCAT GAGTTTTCAA CCTTCCACTT GGTTGATTTA    3000

CCATTTTCGT CCAAGTCAAC ACCTGTCAAG ACCATGGCGT GGGTCATCAA GCTTTCACTA    3060

TAGTCCAAAC GTCCAGCCTT GTCTTGAGTA AGTTTAATGT CCATGCTTGA TTCAAAGTCA    3120

TAAACATCTG TCGCAAGGAT GCCAGCTTAC GGTTGCTGAG CTGGCCGACA TCAGAACCAA    3180

ACCAAACAGT CTCACCTGCT TGCATTTGGG CAATCGCCAA TTCTTTCAAG CGCTCCATTG    3240

GAACGTTGAT GTAGCGAACT GCACGGCTAC CAACCACATT CCCCAACATC TCAACTGTGT    3300

AAGATTTTCC GTAAGGTTTA TCAGCAGTTG GAGCATTGAT AACAGAAACG TAGTCTTCTA    3360

AAGGAAGATT GACATATTTC TTGTAAAACT CTTGTGGTGT GATTCCTTTT TCACTTTTGT    3420

AGTTGTTATC TTTATCGCGA TAAGCAAAGT CAAACTTGCG TGGTGGAAGT CCTAATGACA    3480

TAGCAAGAAA GTTAAAGATT TCTTGCAAGA GGTCTTCTTT CTTAGCTTGA ACAGTCGCTT    3540

GATCTGCACC AGAAACAAGC AAGTCACGCA AGATTTGAGC ATCTTGACGA AGCAATTTAT    3600

TAAGGATCGC ATTTAGCTCA CGACTGCTGC TAGATGAAAC AGACTCAGGA TAAACTGACT    3660

TAGGCACGAC ACCGTATTTT TCAAAGAGGG AAACGACCAT ATCCCATTGA CCGCCATCTT    3720
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1209

GTTGAGGTGT	TTGGAGTAAG	AAGCTAACtT	GCGGCTAGTC	AATTCTTGGT	CTGAAGTCGC	3780
AATGACTTGC	TCCAAGAACC	AGTTTGATTT	CTCATACTTA	TCCCAGAAGA	AAGTGTGGGC	3840
TTGTGACAAC	TCAAAGTTCT	CCAATTTGTA	TTGCGAGATG	AGTTTGTGGC	GGAAGGTGTT	3900
GAGAGCCGCA	AACATCCAGC	AACGACCAGA	CGCTTTCTGG	TTAGTGACCT	TGTCCTTGGT	3960
TAAATCCAAT	GAGAAAACAG	GTGTGTTGTC	TACATGGCTT	TGGCGACGTT	CCAGAGCTGC	4020
AAAAATTCCG	TTGTGGCTGG	CAGCATTTTC	AATCGCTTGG	TATTTTACAT	TTGCTTCATA	4080
GTTGGCAAAT	AGTTTATCAG	TAAATGATTC	TTGAATCGCG	TTCATAGATT	CCTCCTTTTA	4140
GTCTACAGTG	TATTGG					4156

(2) INFORMATION FOR SEQ ID NO: 212:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3902 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA	AAATAAAACA	AAAACAAAAA	TATCGAGGTT	TATTTTCAAA	ACTTTCGATA	60
TTTTTATTAA	GTTATTATTT	TGTTGTTTCT	AGTTTACTTT	TTGATGGTTA	AGAGTGGTGG	120
AGAATTATAC	TCAATGAAAA	TCAAAGAGCA	AACTAGGAAG	CTAGCCGCAG	GCTGTACTTG	180
AGTACGGCAA	GGCGAAGCTG	ACGTGGTTTG	AATTTGATTT	TCGAAGAGTA	TTAGTGCAAA	240
CCGTAGTTGT	AGTCATCATC	TTGCATGGCT	TCAACTTCGC	CAAGAAGGTA	ACCATTTCCG	300
ACTTGAGAGA	AGAAGTCATG	GTTGGAAGTT	CCTGTTGAAA	TACCGTTCAT	AACGATTGGG	360
TTGACATCTT	CAGCTGAATC	TGGGAAAAGT	GGATCTTGTC	CCATGTTCAT	GAGAGCTTTA	420
TTGGCATTGT	AGCGAAGGAA	GGTTTTAACC	TCTTCAGTCC	AACCAACACC	GTCATAAAGA	480
CTCTCTGTGT	AGCCTTCTTC	ATTTTCATAA	AGAGTATAGA	GTAGGTCGTA	CATCCATTCT	540
TTGAGTTTTT	CTTGCTCTTC	TTCAGGTAAT	TCATTGAAAC	CAAGTTGGAA	TTTGTAACCA	600
ATGTAGGTTC	CGTGAACAGA	CTCGTCACGA	ATAATCAATT	TAATGATTTC	TGCAACGTTG	660
GCAAGTTTGT	TGTTACCGAG	ATAGTAGAGG	GGAGTGAAGA	AACCAGAGTA	GAAGAGGAAG	720
GTTTCGAGGA	AGACGCTGGC	AACTTTCTTT	TCAAGTGGGC	TGCCGTTTAG	GTAGATTTCG	780
TTGACAATCT	CAGCCTTCTT	TTGTAGGTAA	GGATTGGTAT	TGGTCCATTC	GAAAATTTCT	840
TCAATCTCAG	CCTTAGTATT	CAAGGTAGAA	AAGATTGATG	AGTAAGATTT	AGCGTGGACA	900

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                                         1210
GATTCCATAA ATTGGATGTT ATTGAAGACA GCTTCCTCAT GTGGTGTACG GATGTCTGCG        960

CGAAGGGCTT GAACCCCAGT TTCAGATTGC ATAGTGTCAA GAAGGGTTAA ACCACCAAAA       1020

ACTTTTCCGA CCAAGTCTTT CTCTTTGTTA GATAGCTTTC TCCAGTCATC CAAGTCGTTT       1080

GATAAGGGAA TACGTGTATC GAGCCAAAAT TGCTCCGTCA GTTTTTCCCA AGTTGATTTG       1140

TCGATGACAT CTTCGATGGC ATTCCAGTTA ATGGCTTTGT AGTAAGTTTC CATTTAAAAT       1200

CTCTTTCTGT GTTTAGTATT GCGAACTCAC AATTATTTCT ACTTTACCAT AATTCTATAG       1260

GAGTATCGCA CAAAAAGTCG GAAGCCCGAC TTTTAAAATG TTACATAAAT TATGTTATGA       1320

CATAGTAGAT TTGATTTTAT CAGTGCTGCT TAGGGAAAAA TAGTGTTTCT ATGCTAGAAA       1380

CTAAATCACA CAGCTTTCAC ATTGGTTGGC GCCGACTTCT CCACCGTCAT CTGTAAAGGT       1440

ACGGACGTAG TAGATAGACT TGATTCCCTT GTTAAAGGCA TAGTTACGAA GGATGGACAA       1500

GTCACGTGTC GTTTGTTTAT TTTCCCTCTT CCATTCGTAA AGGCCTTTTG GAATGTCACT       1560

GCGCATGAAG AGGGTGAGTG AAAGTCCTTG ATCCACGTGT TCAGTCGCAG CAGCGTAAAC       1620

ATCGATGACT TTACGCATAT CCATATCGTA GGCAGAAGTG TAGTAAGGAA TGGTTTCTGT       1680

AGACAAGCCA GCAGCAGGGT AATAGATTTT ACCAATTTTC TTCTCTTGGC GTTCTTCGAT       1740

ACGTTGCGTA ATCGGGTGGA TAGAAGCAGA AACGTCGTTG ATATAGCTGA TAGAACCATT       1800

TGGCGCTACA GCAAGGCGAT TTTGGTGGTA AAGACCATCT TCTTGAACCT TGTCGCGAAG       1860

TTCAGCCCAA TCAGCAACAC CAGGGATAAA GACATTTTTG AAGAGTTCTT TAACACGGTC       1920

TGATGTTGGA ACAAATTCAC CAGTTACATA CTTGTCAAAG TAACTTCCGT TAGCATAGTC       1980

TGATTTTTCA AAGTTGTGGA AGGTAATACC ACGTTCACGT GCAATATTGT TTGACTCTAC       2040

CAAGGTCCAG TAGTTCATAA GCATAAAGTA GATGCTTGTA AATTCAACAG ACTCAGGTGA       2100

ACCATATTCA ATGAGTTGTT GGGCAAGGTA GCTGTGCAGT CCCATGGCAC CGAGACCAAA       2160

GGTGTGGGCT TGGCTATTTC CATGGTCAAT CGTTGGTACA GCTACGATAT GTGAACTATC       2220

TGTAACGAAA GTAAGGGCAC GAACCATAGC ACGGATAGAA CGACCAAAAT CAGGTGAAGT       2280

CATCATGTTA ACCACGTTGG TTGAACCCAG GTTACATGAA ACATCTGTTC CCATTTGAAG       2340

GAATTCTTGA GCATCGTTGA TCAAGCTTGG TTCTTGAACT TGAAGAATCT CAGAACACAA       2400

GTTACTCATG ATAATCTTTC CATCAACAGG ATTTGCACGG TTAGCCGTAT CGATGTTGAC       2460

TACATAAGGA TAGCCAGACT CTTGTTGCAA TTTAGAGATT TCAGTTTCCA AATCCCGCGC       2520

CTTGATTTTT GTCTTGCGAA TATTTGGATT TGCGACCAAT TCATCGTATT TTTCAGTAAT       2580

GTCGATGTAA TTGAATGGCA CACCGTATTC TTTTTCTACA GAGTAAGGGC TGAAGAGGTA       2640

CATTTCTTCA TTTTTACGAG CCAATTCGTA GAATTTATCA GGTACTACAA CACCAAGTGA       2700
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1211

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TAGAGTCTTG ACACGTACTT TTTCATCAGC GTTTTCTTTC TTAGTTGAAA GGAAAGCGAT    2760

GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCCAATTG    2820

GTTGGAGTAA GAGAAGCTGT CTTCAAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC    2880

TCCTTCATAG CCTTTGATAG GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCCAC    2940

ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCCGA TAGAGTTCAT    3000

ATCATCCGTC ACTTGGATTA GGAAACAAGA TACCAACTCC CCACGACGAG CACGTCCAGC    3060

ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTCAT'TGGCAATATC    3120

GATTGCAACA GCTTCATTCC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGGTCTTC    3180

CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTTAAG GCATATTGAT TGTAAAATTT    3240

ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC    3300

TTCCAAGAAC TCTGGACGGT ATTTCTTGAT AAAGGCTGTT TCGATGTAGT TGTGTTCAAT    3360

GAGGTAATTG ATTTTGTCTT TGATTGAATC AAAAACCATA GTGTTTGGAA CTACATTTTC    3420

TTTAAAGAAA GCATCCAAGG CTTCCTTGTC TTTATGAAGC ATGATTTGTC CATTAACAGG    3480

ACGGTTAATT TCGTTATTAA GACGGAAGTA AGTCACGTCT TCAAGATGTT TTAATCCCAT    3540

AAAATTTCCC TTATCTAATT ACAAAGAAA GGCTTCTAAG TTAGCCCTAA AAGCAGTTTC    3600

TTCTGGATGA TGTACTAAGA TTATGCTAAT TGTTTCAGTT TTCCTGGTTG GAAACCTGAA    3660

AAGACTTCAG TTGGTGTTTG GATAACAGGA GCTGCGCTAA AACCGAGCTC TTTAACTTGA    3720

TCGACGTACT CAGGTTGCTC ATCAAGATTG ATTTCACGAT AAGAGACATT ATTACTGTCC    3780

AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTTACCATT    3840

GTGTAACTCC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTTGTCG    3900

GG                                                                   3902
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(2) INFORMATION FOR SEQ ID NO: 213:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2456 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

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TATTGAAGCT ATTGTAGACT ACAAAGATAA GGATTTGCAG TTAGTAGGCG GTGAGACTCA    60

CTGATAACCT AAAAAGGATA GTCAATTATG CTTGTTTACT AACTATTAAC TATGCTAAAT    120
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1212

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CAATTGAGGT TGTTTACATA AAACTCTATA TCAGAGAAGC CTGATATAGA GTTTTTTCTT      180

GCTAGTTTTA GGATTTTTTT GTAAAATAGA AAAAGTGAAG AGAGGTATGA AATGAGCAAG      240

AAAGATAAAA AAATCGAAAT TCAAGTAGCG GATGCCAAAG TTAATGTTGG TAAAGACAGT      300

TTTGAAGGTT ATACATTGAC TATCGGTAAA AAAGTTATCG GAGAAATTGC CGAATTAGAC      360

GGACAATTTG CCATTATAAA GAATGGGAAT GTCGATAGTT TTTATAAAAA ATTGGAAAAA      420

GCTGTGGAAA TTTTGATTGA AAATTATAAT TTAGCAAAAT AAGTCTTGTT TTTTTGAAAT      480

TTTCATGATA TAATAGTCCA TGTTGATTGT AGGAGAGATA GCGAAGAGGC TAAACGCGGC      540

GGACTGTAAA TCCGCCCCTT CGGGTTCGGG GGTTCGAATC CCTCTCTCTC CATTTCATTA      600

ATGGGGTATA GCCAAGCGGT AAGGCAAGGG ACTTTGACTC CCTCATGCCT TGGTTCGAAT      660

CCAGCTACCC CAGTTCTTAG GTAATAATCA AGATAGAAAG CAAAATATCT TAGGGTATTT      720

TATTTTTATA ATTGAAAGAC GTGAATGATA TGAACATGTC CTTGCGGGTG CTTAGGAAAA      780

AAATTATAAG TATGTCAAGT TTAAGAAAAA CTTGATTGTT GGAGGATTTT TTAGATGAAC      840

GAATTTGAAG ATTTGCTAAA TAGCGTTAGT CAAGTTGAGA CTGGTGATGT TGTTAGTGCT      900

GAAGTATTGA CAGTTGATGC GACTCAAGCT AACGTTGCAA TCTCTGGAAC TGGTGTTGAA      960

GGTGTCTTGA CTCTTCGCGA ATTGACAAAC GATCGTGATG CAGATATCAA TGACTTTGTT     1020

AAAGTAGGAG AAGTATTGGA TGTTCTTGTA CTTCGTCAAG TAGTTGGTAA AGATACTGAT     1080

ACAGTTACAT ACCTTGTATC TAAAAAACGC CTTGAAGCTC GCAAAGCATG GGACAAACTT     1140

GTTGGTCGCG AAGAAGAAGT TGTTACTGTT AAAGGAACGC GTGCCGTTAA AGGTGGACTT     1200

TCAGTAGAAT TTGAAGGTGT TCGTGGATTT ATCCCAGCTT CAATGTTGGA TACTCGTTTC     1260

GTACGTAACG CTGAGCGTTT TGTAGGTCAA GAATTTGATA CTAAAATCAA AGAAGTTAAC     1320

GCTAAAGAAA ACCGCTTCAT CCTTTCACGT CGTGAAGTTG TTGAAGCAGC TACTGCAGCA     1380

GCTCGCGCTG AAGTATTCGG TAAATTGGCT GTTGGTGATG TTGTAACTGG TAAAGTTGCT     1440

CGTATCACAA GCTTCGGCGC TTTCGTCGAC CTTGGTGGTG TTGACGGATT GGTTCACTTG     1500

ACTGAATTGT CACATGAACG TAATGTATCA CCAAAATCAG TTGTAACTGT TGGTGAAGAA     1560

ATTGAAGTGA AAATCCTTGA TCTTAACGAA GAAGAAGGAC GTGTATCACT TTCACTTAAA     1620

GCAACAGTAC CAGGACCATG GGATGGCGTT GAGCAAAAAT TGGCTAAAGG TGATGTAGTA     1680

GAAGGAACAG TTAAACGTTT GACTGACTTC GGTGCATTTG TTGAAGTATT GCCAGGTATC     1740

GATGGACTTG TTCACGTATC ACAAATTTCA CACAAACGGA TTGAAAATCC AAAAGAAGCT     1800

CTTAAAGTTG GTCAAGAAGT TCAAGTTAAA GTTCTTGAAG TTAACGCAGA TGCAGAACGC     1860

GTGTCACTTT CTATTAAAGC TCTTGAAGAA CGTCCAGCCC AAGAAGAAGG ACAAAAAGAA     1920
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1213

GAAAAACGTG CTGCTCGTCC ACGTCGTCCA AGACGTCAAG AAAAGCGTGA TTTCGAACTT   1980

CCAGAAACAC AAACAGGATT TTCAATGGCT GATTTGTTTG GTGATATCGA ACTTTAATCA   2040

AATTGAAAAT TCACAAAATC CTTTGTTTAC TAAACAAGGG ATTTTTCTGG CTCTTTGTCA   2100

ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC GAGAAAGGAC AAATTTTGTC CTTTCTTTTT   2160

TGATATTCAG AGCGATAAAA ATCCGTTTTT TGAAGTTTTC AAAGTTCCGA AAACCAAAGG   2220

CATTGCGCTT GATAAGTTTG ATGAGATTAT TGGTCGCTTC CAGTTTGGCG TTAGAATAGT   2280

GTAGTTGAAG GGTGTTGACA AGCTTTTCTT TATCTTTGAG GAAGGTTTTA AAGACAGTCT   2340

GAAAAATAGG ATGAACCTGC TTAAGATTGT CCTCAATAAG TCCGAAAAAT TTCTCCGGTT   2400

CCTTATTCTG AAAGTGAAAC AGCAAGAGTT GATAGAGCTG ATAGTGGTGT TTCAGG   2456

(2) INFORMATION FOR SEQ ID NO: 214:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10974 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA TAGAGACATC CTTCTGATCT GCTTTTwACA AAGTCCAATT ATATGCGGAT   60

CTATACCTCC ACAATGTCCA TTATTATmCC TAACTATAAT ATGAGCCGAA AACACTATAT   120

CCTTAATGTC TCCATATCCA TCAGGGATAT TAATATTTAT TTTTCCACAA CTATATTGCA   180

TTGTAACCAT CTCCTTAAAC GACGCATTAT GATATTTGAT AGAGAAATTT TTATGAATAA   240

CTCAATAATT TTATAGTAAA TCATGCTTAT ATCTCAAAGA TACCTATTTT ATCTTGTCTC   300

GACCTTCTCC AAAGAATTGC TATAATACTA TTACAAATCC ATCTGCACTA CACTTCAAAT   360

TTTAGCACTG TATAAAAACG TTTCAATACA CTAACTTCAA GAAAACTTCC ACTATTAATT   420

GAAAAAATTG ATAGAGATAA ATTAAAAATC TATATTGAAA CTCATCCCGA TGCTTATTTG   480

ACTGAAATAG CTGCTGAATT CAACTGTCCT CCAACAACTA TTCATTACGC TCTAAAGGCT   540

ATGGGATATA GTCTAAAAAA GAGCCGTACC TACTGCGAAC AAGACCCAGA AAAAGTAAAT   600

CGGTTCCTTA AAGAATTGAA TCACTTAAGC TACCTGACTC CTATTTATAT TTATGAGACA   660

GGGGTTGAGA CCTATTTTTA TCTCGAATAT GATCGAGCCT TGAGCAGGCA GTTAGTCTCT   720

CTGGAAGAAG ATATAATTAT TTGAATTAAG ATCGAGACAA CGCACACCAG AGATTGCGAT   780

ACTGTTATAG AAGTACTAAT GCCCTTTTTT GTTTCAATAT ACTATGGCTC CGATGACCTA   840

1214

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TAAAGATACG ATGACGAGTG ACTTTTTCGA AGCTTGCTTC CAAAAATTCT TACTACCTAC        900

TTTAGATACA CCATCCCTTA TCATTATGGA CAATGCAAGG TTTCACAGAA TGAACATGTG        960

TAAGGAGCAG GGCATAGACT GTTACCACTT CCTACCTATT CACCCGAGTA TAATCCCATT        1020

GAGAAAATAT GGGCTTACAT CAAAAACATC TCAGAATAAT ATTGTCAAAT TACGATGCTT        1080

TTCTTGAGGC ACTTTTGTCC TATTCTTGTT TCAGCCGACT ATACTCCGTT ATTGGGCAGC        1140

TACGGAACAG TCGATGGGAC GATGGGGGGA CATAAAAAAA TCCTCCAGTT TTGTTTTTTA        1200

TAACAGTATA CTGGAGAATT GACAATCTCG GTAGATACCT CGTTATAGCG CGGTTACTTA        1260

TTAGGCAGTT ACAAAACAAC TGTGAACAGA AAACATTCCA GAGTCAGACA AGACTTTGGA        1320

ATGTTTTGGC TCTATAATTT CTGTAGTGGG TAATCCCACC CCAGGAATTA TAGGGTCGTT        1380

TCTTGTAGAA AAAAAGCCCC ATATGACCTA TAATGAAAAG CGTCTAACCA ACTCATTAGA        1440

AAGGGTTCAT ATGGAACAAC TTAAGAATAC CACAGATTTG CTCGGATTGG AAGACAAAAA        1500

TATCAAAATC TTGTCTGTTC TGAAATACCA AACCCATCTA GTCGTTCAGG CAAAGTTGGA        1560

TTCCCCCGCT CCTCCTTGTC CTCATTGTCA AGGGAAGATG ATCAAATACG ACTTCCAGAA        1620

AGCCTCTAAA ATTCCGCTTC TCGACTGTCA GGGTTTACCC ACGGTACTGC ATCTCAAAAA        1680

GCGCCGCTTT CAGTGCAAGA ATTGCCTTAA GGTGGTCGTT TCTCAAACAT CCATTGTCAA        1740

GAAAAATTGC CAGATTTCCA ACATGGTGAG ACAAAAAATC GCTCAGCTCC TCCTTGAAAA        1800

GCAGTCTATG ACTGAGATTG CCCACAGATT GGCGGTCTCA ACTTCCACCG TCATCCGAAA        1860

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TGAGTATAGC TTCAAAAAGA GCAAAATGAG CTTCATTGCC CAAGATTTTG AGTCCAAATC        1980

CATCCTCGCA ATTTTAGACG GGCGAACTCA TGCGGTGATT CGAAACCATT TCCAACGCTA        2040

TCAGAGAGAG GTTCGGGAGC TGGTCGAGGT CATCACCATG GACATGTACA GCCCTTATTA        2100

TCGGCTCGCT AAGCAACTCT TTCCAAAGGC GAAGATTGTT CTTGACCGCT TCCACATTGT        2160

CCAACATCTG AGCCGAGCTA TGAACCGAGT ACGAATCCAA ATCATGAACC AATTTGACCG        2220

AAAATCCTTG GAGTATCGGG CGCTCAAGCG CTTTTGGAAC CCTCGCTTTT TCGTTTCTAG        2280

GCTCGGGCTA AATCAGTCCA CTGGACTGAT TTACTACACC AGTATAGCTT CAAGCTCTGT        2340

CAGAAACGAT TCTATCAGCC CACGTTTCGA ATGCACTTAA CCCATCGGGA AGTACGAGAT        2400

AAGCTGCTTT CTTACTCTGA GGGATTACAG GTTCACTACG AACTCTATCA ACTCCTGCTC        2460

TTTCATTTTC AAGAGAAGAA TGCCGACCAT TTCTTTGGAT TGATTGAGCA AGAACTGCCA        2520

ACGGTTCATC CGCTTTTTCA AACGGTCTTT TGGACTTTTT TAAGGGATAG AGATAAGATT        2580

ATCAACGCAC TTAAGCTGCC TTATTCCAAC GCTAAACTTG AAGCGACCAA TAATTTGATT        2640
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1215

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AAGATTATCA AGCGCAAAGC CTTTGGTTTC CGGAACTTTA ACAATTTTAA AAAACGGATT        2700

TTGATGACTT TGAACATCAA AAAAGAGAGT ACGAATTTCG TACTCTCCAG ATTGCAGCTT        2760

TTCGCCTACC CACTACACTT GACAAAGAGC CACTCTTTAT TCCATGGTAT CAAAGGCAAG        2820

ACTTGGTTTG GCATTGAGGT CCCAGCCTGC GAAGTTTTCT TTGTTCCACT CGCTGACGCT        2880

GGCATAGGCA ATCATACCTG CATTGTCTCC GCAGAGTCGC AGAGGGGGGA TGATAACCTT        2940

GACATCTGTG ATTTCGGCTG CTAGGCGTTC TCTGAGACCT TTATTGGCTG CCACACCACC        3000

TGCCACAACT AGGATTTTAA CAGGATATTT CTCCAAAGCC TTCTTGGTTT TTGCCATGAG        3060

AATGTCCATA ACTGCTGCTT GGAAGGAAGC ACACAAATCT TCTGTAGACA GGCTTTCTCC        3120

CTTTTGCTCG GCATTGTGAT GAAGATTGAT AAAGGCAGAT TTCAAACCTG AGAAGGAGAA        3180

CTCCAGATTA TCTTCCTTAA TCATGGCACG GGGGAAATCA TAAATATCCT GCCCCTGATG        3240

AGCCAGCTCG TCAATCTCAC GACCTGCAGG ATAGGTCAAG CCCATGACAC GGCCGACCTT        3300

ATCATAAGCC TCACCAACCG CATCATCACG GGTTTCCCCA ACAATCTTAT AATCTCCTGC        3360

CTCCGAAACA TAAACCAACT CTGTGTGTCC GCCGCTGACC AAGAGGGCTA GCAAGGGAAA        3420

CTCCAAAGGC TCCACACTCT GAGCTGCCAT GAGGTGCCCA GCCATGTGAT TAACAGGAAT        3480

CAGTGGAAGT CCGTGAGCCC AAGCAAAGGC CTTGGCAGCT GACAAACCAA CTAGCAAGGC        3540

TCCGACCAAG CCTGGTCCGT AGGTAACCGC AACAGCTGTC ACGTCCTCTT CGGTAATCCC        3600

TGCTTCTGCC AATGCCTCCT CGATACAGGC TGTAATGACC TCGACATGGT GACGACTGGC        3660

TACTTCGGGC ACTACGCCAC CAAAACGTTT GTGACTCTCA ATTTGACTAG CAATGACATT        3720

GGACAAGAGC TCATCGTCGT TTTTCAAGAC GGCGACACTG GTCTCATCAC AGGATGTCTC        3780

AAATGCTAAA ATATATCTAT CCTTCATCTA TTTCTCTCTT CATGATAATG GCGTCCTCGA        3840

CTGGGTCATG GTAGTAGGCC TTTCGCTCAG CGATAACTGT CATCTTTTCT TTCTTGTAAA        3900

ATGCTTGCGC TCGTTGATTT GACTGTCTGA CTTCGAGGAA AATTTCCTTG TCTGTCGGCA        3960

ATTGAGCAAA CAAGGCTGAC GCAATCCCCT GACCCTGATA AGCTCCTTTG ACAGCGATTT        4020

GCAGGACTTC TGCTTCAAAA AGATTCTCCT GCACAGCTAG AAATCCAATC ACTTCTGCCC        4080

CATCATAAGC CAATGCATAC CAAGTCTGGT CTTGGGACAG ATCTGCTTGG ATTTGCTCCA        4140

GAGTCCAAGG ACTGACTAGG TAAACAGCTG CCATAACAGC GTAGATGGCT TGAGCTAGGT        4200

CAGGCTGTTG TTGAATTCGC TTGATTTCTA TCATAGGCGT TTAATGTAAG ACTCGCCAGA        4260

CTCGGTATGG TTCTTGAGCC AGTTTTCCTC AGCCTCGACT CGTTTGAGGT AATTCGGCAC        4320

AAAATCATGC AAGGAGTCTG CTTCCTTGTC CCAGGCCAAA AGAGCTAGAT TAGCTGCATT        4380
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1216

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GGGCAATGTT TCTTTGTAAT CAGTCCTTGG CAAGTGTTTT TGAATCTGCT CAACAAAGGG    4440

GCCAACTTCT CCGACAAAGG TTACCTGACT AGTACCCTTG ACTTTTTCTA GCACCTCTTC    4500

AAAAGATAGG TGCGCTTCTG CCATGACAGG TTTGGCATTT TCATAAAATC CTGCATAAAC    4560

ATTATTGCGA CGCGCATCCA TCAAGGGGAC AAACAAACCT TCTTGTTGAT GGGGCACCAG    4620

AGCCAAGAGA CTCGACATAC CAACCAACTC GATGTTCAGG GTGTGAGCTA AGGTCTTAGC    4680

AGTTGCTACC GCAATTCGCA AGCCTGTATA GCTACCCGGC CCTTCAGCTA CCACGATTCG    4740

GTCCAAATCC TTGGGTGTCC AATCCAAACT TGCCATCAAA AAATCGATGG CAGGCATAAG    4800

AGTAATACTG TGATTTTTCT TAATATTAAT CGTCGTCTCG GCAAGAACCT GCTTATCCTC    4860

TAAAATAGCC AGAGAAAGAG CCTTGCTGGA CGTATCAAAA GCTAATACTT TCATAACACA    4920

TTCCTATCTT TTTGTCTGCT TACTATTATA CTACAAAAGC TGGCACATGG GAATTTTCTT    4980

TGCCCCCAGA CAAGAGTGCC CTCACTTAAC TAAAAATAAT TTAAAAAAAT GCTCACTTTT    5040

CCTTTTCTTT TCCGAATATA AAAGTGAACA AGAAAAAAGG AGGAAAGTTC AATGACAAAT    5100

TTTGACATTC TTGACAATCA ATTTTTATCC TTATCTGAAA ATGAATTATC AGATATTGAT    5160

GGCGGTCTCG CTCCCTTGGT TATCTTTGGA GTAGCAGTAT CTTGGAAGGC TATTGCAGGT    5220

GGAACAGCAC TTATAGGTTC TGGTTTGGCA GCTGGTTATT TTTTAGGAGG AGATTAATAT    5280

GATGAAAGAT TTGAACAATT ATCGTGAAAT TTCTAATAAG GAATTGCAAG AAATCAAGGG    5340

TGGCTTTGGT GTCGGTGTTG GTATCGCTTT ATTTATGGCA GGTTATACCA TTGGAAAAGA    5400

CCTTCGTAAA AAGTTTGGTA AGTCATGCTA GATAAGAAAC ACATTTTTAG AAGGATAAAT    5460

TTTATTGTCT TCATCTCTTA CAGTTTGCTC AGCATTCTCA ATGATTTGAA CATTACTACC    5520

ATCCCTTTAC CATTCGATTT ATCTGTTTGT ATTGTTTTAT TTTTATGCTT CAACTCTATT    5580

TTTGATCAGA ACAATGACTC CCATAAAAAT AATAAGCTTT GAAAATTCCA TTGTCATGTC    5640

ATGTTAGAAA AATGCAAAGA CCACCTCATC TTGATAGATG GGGTGGAATT TTCGTGTCGT    5700

AAATCTACTA TCTCTACATT CCCAAACAAA AAACCCCAGC ATAAGCAGGG CATCTAAGCA    5760

TTTAATTCAA AGTAAAATAC AAACCAAACG ACATAGGTCA CGAGGAGGAG AAAAAGCGAG    5820

TAGAGAGTCA CAAAGGTCAT TTTCCACAAG AACTTGGTTT GTCGTCGTTC CAGTTTGGCA    5880

AATAGAAGAT TCCCCGCATA AACGCAAGCA ACAAAAACAA TAAAAGCTAC CAAGCGAGCT    5940

CCGATAGCAA AAGCAAATAA GTTATACATA GGGCAACCTC CTTGACTTAA AATCTATATG    6000

GAATTATGAC AAGCAATAAA TTTCACTTCC GTTATCAACA TAATACATTT TCTTTATTTT    6060

TGAAAACGCT TACCAAAGAA ATCGTCCCCT AACTTTCTCG TTTCCGTCTT TTACTAATTT    6120

TTCATTTTGT GGTATAATTG AAATAATTGT AACGAATCAA GGTCAATCTA GACACAAAAT    6180
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1217

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GGAATGAAAT CAAGCAAATA TCTGCTAAAA GTTTGGAATA AGCTGACCTG TAAATAGAAA      6240

GGAACTATAT GATTTACAAA GTTTTTTATC AAGAAACAAA AGAACGTAGC CCACGCCGTG      6300

AAACAACACG CACGCTTTAC CTAGACATCG ATGCCAGCTC AGAACTTGAG GGCCGTATCA      6360

CTGCTCGCCA ACTTGTCGAA GAAAATCGCC CAGAGTACAA TATCGAGTAT ATCGAACTCT      6420

TGTCTGACAA ATTGCTCGAT TACGAAAAAG AAACTGGCGC CTTCGAAATT ACGGAGTTCT      6480

AATATGGCCT ACACTCTTAA ACCTGAAGAA GTCGGCGTTT TTGCCATCGG TGGTCTAGGA      6540

GAAATCGGGA AAAACACTTA CGGAATTGAA TACCAAGACG AGATTATCAT CGTCGATGCT      6600

GGGATTAAAT TCCCAGAAGA TGACTTGCTT GGTATCGACT ATGTCATTCC TGACTACTCT      6660

TACATCGTGG ACAATATCGA CCGCGTCAAG GCTGTTTTAA TCACACACGG ACACGAGGAC      6720

CACATTGGTG GGATTCCGTT CCTACTCAAG CAAGCAAATG TCCCTATTTA TGCTGGACCG      6780

CTTGCCTTGG CTTTGATCCG TGGGAAACTC GAAGAACACG GCCTCTTGCG CAACGCCAAA      6840

CTTTACGAAA TCAACCACAA CACCGAGTTG ACCTTTAAAA ATCTCAAGGC AACTTTCTTT      6900

AGAACGACTC ACTCTATTCC AGAGCCTTTG GGGATTGTCA TTCATACTCC TCAAGGGAAA      6960

ATCGTCTGTA CGGGTGACTT TAAGTTCGAC TTTACTCCAG TTGGAGAACC TGCCGGACTTG      7020

CATCGTATGG CTGCGCTTGG TGAAGAAGGC GTGCTCTGTC TCCTGTCTGA CTCGACAAAT      7080

GCGGAAGTAC CAACCTTTAC CAACTCTGAA AAAGTCGTTG GTCAGTCCAT TATGAAGATT      7140

ATCCAAGGTA TTGAAGGACG TATCATCTTT GCATCCTTTG CCTCAAATAT CTTCCGTCTC      7200

CAGCAGGCAA CAGAAGCTGC TGTTAAGACT GGACGCAAGA TTGCGGTCTT TGGTCGTTCT      7260

ATGGAAAAGG CCATTGTCAA CGGAATCGAT CTTGGCTACA TCAAAGCTCC TAAGGGAACC      7320

TTTATCGAGC CAAATGAAAT CAAAGATTAT CCTGCAGGAG AAGTTCTTAT CCTCTGTACA      7380

GGTAGTCAGG GTGAGCCTAT GGCAGCCCTC TCTCGTATCG CCAACGGAAC CCACCGTCAA      7440

GTACAATTAC AACCAGGTGA TACCGTTATC TTCTCTTCTA GTCCCATCCC TGGAAACACT      7500

ACTAGTGTCA ACAAGCTGAT TAACATCATT TCTGAAGCTG GTGTCGAAGT TATCCACGGT      7560

AAAGTGAACA ATATCCATAC ATCTGGACAC GGTGGTCAGC AAGAGCAAAA ACTCATGCTC      7620

TGCTTGATTA AGCCAAAATA CTTCATGCCT GTCCACGGTG AATACCGCAT GCAAAAAGTC      7680

CACGCTGGAC TAGCAGTGGA TACTGGTGTT GAGAAGGACA ATATCTTTAT CATGAGCAAT      7740

GGCGATGTGC TTGCCCTTAC TGCTGACTCA GCTCGTATCG CAGGTCATTT CAACGCCCAA      7800

GATATCTATG TCGATGGAAA TCGTATCGGT GAAATTGGCG CAGCTGTCCT CAAAGATCGT      7860

CGCGATCTAT CTGAAGACGG TGTCGTTCTG GCAGTTGCAA CTGTTGACTT CAAATCGCAG      7920
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1218

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ATGATTCTAT CTGGTCCAGA CATCCTCAGC CGAGGCTTTG TCTACATGAG AGAGTCTGGC      7980

GACTTGATTC GCCAAAGCCA GCGTATCCTC TTCAATGCCA TTCGTATCGC ACTGAAAAAT      8040

AAGGATGCTA GCGTGCAATC TGTCAATGGT GCCATTGTCA ACGCTATTCG CCCCTTCCTC      8100

TATGAAAATA CCGAACGTGA ACCGATCATC ATCCCGATGA TCCTCACACC AGATGAAGAA      8160

TAAAGCAAGA AAACAGCCCC GTCCTCGGAG CTGTTTTTCT CTATGCTTTC TTTTGAGATT      8220

AAAACTCATA CTCAATGAAA ATCAAAGAGC AAACTAGGAA GCTAGCCGTA GGTTGCTCAA      8280

AGCACTGCTT TGAGGTTGTA GATAGAACTG ACGAAGTCAG TAGCCATACC TACGGCAAGG      8340

CGACGTTGAC GCGGTTTGAA GAGATTTTCG AAGAGTATCA ATAAAAATCG AAATCAGACT      8400

AGAAGGCTAA GCGAAAGCAT AACTTGAGTT AGCTCCCATA GTTCGGGAAA CTATGGGAGG      8460

CTGGAGATGA ATCAAAGCCA AGCTTTGAAC TCATTCGTAA GAAGCCGACG ACGTATCATT      8520

TTGATTTTTG AAGAGTTTTA GAAATACTAC GATTTTTACC TTCCAGATAC ACCATCAAAA      8580

TAGAAATATC TGCTGGGTTT ACTCCCGAAA TACGGCTGGC TTGGCCGATG GTTTCTGGAT      8640

TGATGAGTTT GAACTTCTGA CGGGCTTCGG TTGCGATAGA ATCAATGTCA TCCCAGTCGA      8700

TATTGGCCGG AATGCGTTTT TCTTCCATGC GTTTCATCTT GGCAACCTGG TCCATGGCTT      8760

TGGAAATATA GCCTTCATAC TTGATTTCTG TTTCAATCAA TTCGATAATC TTGTCATCCA      8820

AGTCTTCTGC AGCTGGTCCG ATGAAGGCCA CCACATCTTG GTAAGAAACT TCTGGACGGC      8880

GAAGGAATTC CTTGGCTGTC ACTGCATCGG TCAAGGGTTT GAAGCCCATC TCCTCAACCT      8940

TGGCATTGGT TTCCTTGACT GGCTTGAGTT TGATACTGTC TAGGCGCTTC ATCTCATTAT      9000

CAAATTGATT TTTCTTGATT TCAAAACGAG CCCAGCGTTC ATCGTCCACA AGGCCAATCT      9060

CGCGTCCCAT CTCAGTCAAG CGCATATCAG CATTGTCATG ACGAAGAATG AGACGGTATT      9120

CAGCACGACT GGTCAAGAGA CGGTAGGGTT CAATGGTTCC CTTGGTCACC AAGTCGTCGA      9180

TCATCACCCC GATATAACCA TCACTGCGCT TCAAAATCAA TTCAGGCTTG CCTTGGATTT      9240

TCAGAGCCGC ATTGATACCC GCGATAATCC CTTGGCCTGC TGCCTCTTCG TAACCTGATG      9300

TTCCATTTGT CTGACCAGCA GTGAAGAGAC CTGAGATTTT CTTGGTTTCC AAAGTCGCAC      9360

GCAACTGATG AGGCAAGACC ATATCATACT CAATAGCATA ACCTGTCCGC ATCATCTCTG      9420

CATTTTCCAA ACCTTTGATG GAATGCACCA AGTCACGCTG GACATCCTCA GGCAGACTGG      9480

TTGAAAGTCC TTGCACATAG ACTTCCTCAG TATTGCGCCC TTCTGGCTCA AGGAAGAGTT      9540

GGTGACGTTC CTTGTCCGCA AAGCGCACAA TCTTGTCTTC AATCGACGGA CAGTAACGAG      9600

GCCCCACTCC CTTGACCACA CCTGTAAACA TAGGCGCACG GTGGAGGTTG TTTTGGATAA      9660

TCTCATGACT GGTACCATTG GTATAGGTCA ACCAGCATGG TACTTGGTCC TTGACATAAT      9720
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1219

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CCTCATCACG TGAAGTGTAT GAGAAATGAT TAGGCACTTC GTCTCCTGGC TGAATTTCTG    9780

TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC    9840

CGATTTCGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT    9900

TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTTC CCCACGGAGA GCAGTCCCTG    9960

TCGTCACAAT AACAGCCTTA GCAGCATATT CTTGATGGGT GGCTGTACGC ACACCGACAA    10020

CCTTGCCATC TTCCACCAAA ATCTCATCAA TCATGGTTTG ACGAAGGGTC AGATTTTCTT    10080

GGTTTTCAAC CGTCTTGCGC ATCTCCTTAG AGTAAAGTTC CTTGTCAGCC TGCGCACGAA    10140

GGGCACGGAC AGCTGGCCCC TTCCCTGTGT TTAGCATCTT CATCTGGATG TAAGTCTTGT    10200

CAATGGTTTT GGCCATCTCG CCACCGAGGG CATCGACTTC ACGCACGACA ATCCCCTTGG    10260

CAGAACCACC GATAGAGGGA TTACAAGGCA TGAAAGCCAG CATTTCAATA TTGATGGTCG    10320

CAAGCAGGAC CTTACAGCCC ATACGGCTAG CGGCCAAGGA AGCCTCAACC CCAGCGTGTC    10380

CCGCACCAAT TACAATAATA TCGTATTCTT CAGTAAAATG ATAAGTCATG TTTCTCTCCT    10440

ATTCCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCCAATC TGGTAGGGCT GTTTTTAAAA    10500

AGACTGGAAC TAGCTGGATA TTCTGGAGCT TATCCAAGTC AATCCACTCA CAGGGCTGCC    10560

TTTTCTCATC TTCCTGCATG GTCAACGGGG CATCTTCAAG CAAATCCACC AGATAATGAA    10620

ACTCGATATT GTGATAGGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC ACAAAAGCTA    10680

GCTGCCCAGC TTGAGCTTTG ACACCCAGTT CTTCCTTCAC TTCACGGACT ACCGCGTCTT    10740

CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGTA ATACTTGCCC TTGTCTTTGG    10800

TAACTAGAAG CTTGTGATTT TGGACAATCA AGGCTGTAGC CCGAACACCA AAAACCGTAT    10860

TGTCTACTTT TGTCCGAAAG TCTTGTTGAG TCATTCTTGT CCTTTCCCTT AAACGACACA    10920

AAAACAGTCA AAACTACAAA GAAGTGCAGG ACAAAAAAGC CTGCAACATC CAGG          10974
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(2) INFORMATION FOR SEQ ID NO: 215:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 987 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

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CCCGTTATGA TTATGGATAG CGCTTTCAAA TTTTTAAACT CCTATCCCAT CCTTTTATCT     60

ATATAATAAG TGAAAATATA ATAACTGTCA AGTAACTGAA GTGAATTTTA TAAAAAAATT    120
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                                        1220
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ACAAGCCAAA TTTGTAAAGT TTACACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG    180

TTTATTTGTC AATAATCCGA GAAAATCTTG CAACGCTTAG AAGTCTATAA AAACTATCAA    240

CATTTATATG ACTTGCGAAT AGCAATCCTG CTAAACCTTT CCACACTCTA TCTATACAAT    300

CAAGATAAAA ACATGTGTAA GCAAATCTGC TACACTTTAC TGGAGGACGC CAAGAATAAG    360

AAAAGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTTGTAC AGACGATTCT    420

AAACTTATCC AAAAAGGGTT CTCCCTTCTG GAGCTGACCG AGGAAACTTC TATGCTGTCT    480

CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG    540

GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTTAA CGAGAAAGTA TGACTTTTAC    600

GTTTATCCCA ACTCAATTAT GACATTTTTT TCAAAAGTCA ATATATCTCA CTTTTTCAAC    660

GACAAGAAAG AGGCTGATAA TCTACCAACC TCTTATTCTG AACCCATCAC TCCATCACTT    720

TTTAGCTTCA TTCGCTTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATTCCCCTT    780

ACCGGTACAA CCATGAGCAA TTGTAGTCGC TCCTATCTGA TGCGCTATTT CAACCAATTT    840

TTTAGAAATC AGAGGGCGGC TCAAGGCAGA TACCAAGAGA TACTTTTGTT CATAATAGGC    900

ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAAT TCGTCCTTAA CATCAATGAC    960

ATAAGATTCT ACTGCCCAAA CCTTAAG                                       987
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(2) INFORMATION FOR SEQ ID NO: 216:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2651 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:
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CTGGGTCTTG TTCATAGTAG GTGTGGTtCT TTTTTTCGAG TGTAGCCCAT AGCTTTGAGC     60

GCATAGTGGA TGGTAGTTGG ATGACAGCCA AAGTCAGAAG CTATTTCAGT CAAATAAGCA    120

TCTGGATTGT CAGTAAGATA GTTTTTAAGT CTATCTCTAT CAACTTTTCT TGGTTTTGTT    180

CCTTTTACTT GGTGGTTTAG CTCTCCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG    240

GTATTACGTG AGATTTGGAA AACGTGTGAT GCTTCTGTTA TACTACCTAT TCGCTCACAA    300

TAAGAGAGAA CTTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT    360

GTGTACTATT TTTGGTTCAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAACTT    420

CAAAGCACTA TAAAGTAAAT TGAAACAAGA ACAATACAAA CAATTCTCGT AAACGGATTG    480

CAACCACAAA AAAGCAAGCA TTCACAAGAA TACTTACCTA TCATGGGAGG AACAACCGTT    540
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1221

CCTCTTTTTT ATTACTAAAA TTCAAAGAAT TCCAATGCTT TTTTCAAGAG CAAATCCGTA   600

TATTCTGGAT CTTCTTGGGC TACTTCTATT TCCCGCTGAA CTTTTTCCAA ATCATCTGTA   660

ATCACTCCAT CTACTCCTAA GTGAAGAGAT TTGCTGATAG CTTCTGAATC ATTGACAGTC   720

CAGACATAAA GTTTCTGATC CGTTGTCCAT AGTTTGCTTA CAAAATATTC ATCCAAGGTT   780

GAGTACTCCA TAGTATATCC TGTCGCTCTT GTTTTAGGAA AGACAGAATT GTAGGGCATG   840

ATGAAATAAA CTGGTAGTTC GGCATCATAC TGTCTTACTT TTTCGACAAC ATGGTAGTCT   900

AAAGACTGGA TTTGATGTCC ATAAATCTTG AGCTTTGCAG CATAACGGGC TAAAAAGCGG   960

TTCATCATGT CTGGACTATC TTTTTTACTG GTTTTAATTT CAATTAGTAA TTTTTGACCA   1020

AGTTCGTTGG CTCGACTGAG ATAATCTTCA AAGCTTGAAA TTTTAGTCTG GTAGCCATTT   1080

TCAAAAATAT CAATCCCTTT AAGCTCCTCC AAGTTTAAGT CTTGAGGACT TTTATTGATA   1140

CCTGCTAGAT TTTTCAAGTT AGCATCATGC ATCATGACAA ACTGCCCATC TTTTGTTTCC   1200

TGCACGTCCG TCTCCACCAA GTCTGGTTTG AGTTGTGCTG TAGTTTCCAA GGACTCTACT   1260

GTATTTTGAA TCCCATTTGC ATTGGAAACC CCTCGGTGAG AAATAAGTTG AGGTAGATGA   1320

ACCATGGGAG CCTCCAGATA AATATAACCT TCTAAGGCAA AGAAAAGACT GGCACAAGTC   1380

ATGACACCCC ATCGCACGAT GTGATCTTTT TCTCTCCTAG GAAGCATATC CAGCTCCTTT   1440

CCTGTCAAAA ATGAAACAAA TTTAACCAAA AAATAAGTCA GAGCCATATA ATAGAGATTT   1500

TTAATCACGA CAAAATTCAA AATACCAAGA ATCAGAGACT CTCTCTGAGT GATATCATCT   1560

ACCAAAGTTT GAGCCAATAA TAAAGGAATC AAAGGAAGAT ArAATAATAA ATGTGCTTTG   1620

AGCAAGATGT AAAATAAATT CCAAGCATAA AAAGTAACTC TCTTCTTGGT TTTCTCCAAG   1680

CTAAACATCA CTGCTTCTCG AACAGTCAGC TGATCATATA CAATCTTCGG AAGGGCAAAC   1740

ATCAATCTGA CAGAGACATA GAGAAAGATA AGAGATAGAA GTAGGATGCT CAGCCACCAC   1800

ATCCAATATC TATCTTCTAA ATAAGCTTGG ATAAACTCTG GAATGACGAT TTTATTAAGA   1860

TAATAAATCT TCAGCATTTT CCGTATAAAA GGAAACAGCA TAGCTATATA GAAAAAGATA   1920

AACAAGGCTT TAGCGCAAGT TAGCTTTTTC ATAAATCCAA AACTTTCATG GAAAACCTTG   1980

CGGATATACT CAATTAGCCT TCGCTTTTCA TTATAGAGGA GATGACGAGC ACCAATAAAG   2040

AGGAGTCCTA TTTGAAAATA AGCAACCAGA AGGTTAATTA CAATCAAGGC TAAAAAAGCT   2100

AGACTAATCA ATGGAGAATG AGTAAGGATG GCTAAGACAT TGTTATAGGA AATAAAAAGA   2160

TAACCTGTCT GATCTAATAA GAAGCTAGCC AACCATGAAT TGAATGGTAC CCACAAATAC   2220

TCCACTATCA TAAAAATCAA GAAAAATAGA AAGAGGATTT TATCAAGATC GAGGTAAATC   2280

1222

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TGTTTAAGAC CCAATTTTTT AGGTTTTTCA GGTTTCATAG GCACTCCTAG TCAAATAATT    2340

GAGACAAGTC CAAGCCACCA AAAGGATTGT TTGATAAGCT ACTTTCTGTC TCTAACAATT    2400

CCCTAGCTTG ATCCGACTCT AAGAAGGATT CGTAAACACG CGCCGTCATC CGAGCATCCT    2460

CTAAACTATT ATGAGACTGA CCTTGAAATC CAAGAAATGA GGCAACAGTT TGCAATTTGA    2520

GATTGGCAAT ACCATGTAAA TCTGAACTCC GACGTTCAAA AGCTTCATCA TACAAATCCA    2580

CCTTGTACTG TTGGCTATAG TCTAAACCAT GCTCTGCTAA AATAGGTAAA TCACTTTTAG    2640

CAGCATTGTA G                                                        2651
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(2) INFORMATION FOR SEQ ID NO: 217:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5638 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

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CGTTATAATA AACTTGTGAA AAAATTAACA AAGGATATCG TTCCTTGAAA GCTATGGAGG    60

AAAATATGGC TGATAAAAAA ACTGTGACAC CAGAGGAAAA GAAACTCGTT GCTGAAAAAC    120

ACGTAGATGA GTTGGTTCAA AAAGCTCTAG TTGCCCTTGA AGAAATGCGT AAATTGGATC    180

AAGAACAAGT TGACTACATC GTTGCCAAAG CATCAGTAGC AGCTTTGGAT GCCCACGGAG    240

AATTGGCTTT ACATGCCTTT GAAGAAACAG GACGTGGTGT ATTTGAAGAC AAAGCAACTA    300

AGAACTTGTT TGCCTGTGAA CACGTAGTAA ACAACATGCG CCACACTAAG ACAGTTGGCG    360

TTATCGAAGA AGACGATGTA ACAGGATTGA CTCTTATTGC TGAACCAGTT GGTGTTGTTT    420

GTGGTATTAC TCCAACAACA AACCCAACAT CAACAGCAAT CTTCAAATCA TTGATTTCAT    480

TGAAGCACG TAACCCAATC GTCTTTGCCT TCCATCCATC AGCACAAGAA TCATCTGCTC    540

ATGCAGCTCG TATCGTCCGC GATGCAGCTA TCGCAGCTGG TGCTCCTGAA AACTGTGTGC    600

AATGGATTAC TCAACCATCT ATGGAAGCAA CAAGTGCCCT TATGAACCAC GAAGGTGTTG    660

CGACAATCCT TGCAACAGGT GGTAATGCCA TGGTTAAGGC GGCTTATTCA TGTGGTAAAC    720

CAGCTCTTGG GGTAGGTGCC GGAAACGTTC CAGCTTATGT TGAAAAATCA GCAAACATTC    780

GTCAAGCAGC ACACGATATC GTCATGTCTA AATCATTTGA TAACGGTATG GTCTGTGCAT    840

CTGAACAAGC AGTTATCATT GATAAAGAAA TTTACGATGA ATTTGTAGCA GAGTTCAAAT    900

CTTACCACAC TTACTTTGTA AACAAAAAAG AAAAAGCTCT TCTTGAAGAG TTCTGCTTCG    960

GCGTCAAAGC AAACAGCAAA AACTGTGCTG GTGCAAAATT GAACGCTGAC ATCGTTGGTA    1020
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1223

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AACCAGCAAC TTGGATTGCA GAACAAGCAG GATTTACAGT TCCAGAAGGA ACAAACATTC    1080

TTGCTGCAGA ATGTAAAGAA GTTGGCGAAA ATGAGCCATT GACTCGTGAA AAATTGTCAC    1140

CAGTTATTGC AGTTTTGAAA TCTGAAAGCC GTGAAGATGG TATTACTAAG GCTCGTCAAA    1200

TGGTTGAATT TAACGGTCTT GGACACTCAG CAGCTATCCA CACAGCTGAC GAAGAATTGA    1260

CTAAAGAATT TGGTAAAGCT GTTAAAGCTA TTCGTGTTAT CTGTAACTCA CCTTCTACTT    1320

TTGGTGGTAT CGGGGACGTT TACAATGCCT TCTTGCCATC ATTGACACTT GGATGTGGTT    1380

CTTACGGACG CAACTCAGTT GGGGATAACG TTAGTGCCAT TAACCTCTTG AATATCAAAA    1440

AAGTCGGAAG ACGGAGAAAT AACATGCAAT GGATGAAACT TCCTTCAAAA ACATACTTTG    1500

AACGTGATTC AATTCAATAC CTTCAAAAAT GTCGTGACGT TGAACGTGTC ATGATCGTTA    1560

CTGACCATGC CATGGTAGAG CTTGGTTTCC TTGATCGTAT CATCGAACAA CTGGACCTTC    1620

GTCGCAATAA GGTTGTTTAC CAAATCTTTG CGGATGTAGA ACCGGATCCA GATATCACAA    1680

CTGTAAACCG TGGTACTGAG ATTATGCGTG CCTTCAAACC AGATACCATC ATCGCACTCG    1740

GTGGTGGGTC TCCAATGGAT GCTGCCAAAG TAATGTGGCT CTTCTACGAG CAACCAGAAG    1800

TGGACTTCCG TGACCTTGTC CAAAAATTCA TGGATATCCG TAAACGTGCC TTCAAGTTCC    1860

CATTGCTTGG TAAGAAGACT AAATTCATCG CGATTCCAAC TACATCTGGT ACAGGATCTG    1920

AAGTAACACC ATTTGCCGTT ATCTCTGATA AAGCAAACAA CCGTAAATAC CCAATCGCTG    1980

ACTACTCATT GACACCAACT GTGGCAATCG TAGATCCTGC TTTGGTATTG ACAGTTCCAG    2040

GATTTGTTGC TGCTGATACT GGTATGGACG TATTGACTCA CGCGACAGAA GCATACGTAT    2100

CACAAATGGC TAGTGACTAC ACTGATGGTT TAGCACTTCA AGCCATTAAA TTGGTCTTTG    2160

AAAATCTCGA AAGCTCAGTT AAGAATGCAG ACTTCCACTC ACGTGAGAAA ATGCATAACG    2220

CTTCAACAAT CGCTGGTATG GCCTTTGCCA ATGCCTTCCT AGGTATTTCT CACTCAATGG    2280

CCCATAAGAT TGGTGCGCAA TTCCACACAA TCCACGGTCG TACAAATGCT ATCTTGCTTC    2340

CATACGTTAT CCGTTACAAC GGTACACGTC CAGCTAAGAC AGCAACATGG CCTAAGTACA    2400

ACTACTACCG TGCAGATGAA AAATACCAAG ATATCGCACG CATGCTTGGA CTTCCAGCTT   , 2460

CTACTCCAGA AGAAGGGGTT GAATCTTACG CAAAAGCTGT CTACGAACTC GGTGAACGTA    2520

TTGGGATCCA AATGAATTTT AGAGACCAAG GAATTGACGA AAAAGAATGG AAAGAACATT    2580

CTCGTAAATT AGCCTTCCTG GCTTATGAAG ACCAATGTTC ACCAGCTAAC CCACGTCTTC    2640

CAATGGTAGA CCATATGCAA GAAATCATCG AAGATGCATA CTATGGCTAC AAAGAAAGAC    2700

CAGGACGCCG TAAATAATTG TTTATCAGTC TAGAAGCAAG ACAAAAACTC AATTTGAGGG    2760
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1224

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AAAGATCCAG TAATTTTTCT ATGATAAAAG GCATCCTATC AAGGTTTTTG AACACCTGAT    2820

AGGATGCCTT TTTATGATAT TGAGGCCTTT TTGCCCTTTT TGAAAAACTA GAATAGAAAC    2880

AAAATATATA ATAGATTGAA ACTAGAATAG TACATATCTG CTTCTAAAAC ATTGTTAGAA    2940

TTCGATTTGA CTGTCCTGAT CGATTTGTCC TGTTCTTATT TCATTTTGAT ATATAAAAAA    3000

TATAGTATAG TAGACTGAAT CTAAAATAGT ACGAAACAAT TGCTAAAACA TTTATAGAAA    3060

TTAATTTTAC TTTTCTGATA GAGTTGTTCA CATCTTATTT CAATTCACTA TAGTTTAATT    3120

TAAGAGTAGT ATTTACTAAG GCCCAATTAA AATCAAAGAG CAAACTAGAA AACGAGTGCC    3180

ATTCAGCTCA AAACACTGAT TTGAGATTGC AGATAAGACT AGCCCCCTCA TTAACAGATT    3240

TACGATAAAA CGATGACAAG GTGTGTTGCT TTTTGATTTC TAAAGAGTAT AATGATAGAT    3300

CTCTATAAAA TAAGTGCGAA GGAAATGAGC TTTTATAGTC CTTTCGTTTT AAAATACTAT    3360

CTCAGATATT CTTATATCGA CAAGAAGTTT TTGAGTCATT CCCTCATCAT ACATATTAAA    3420

TAAATAGTGG CTCATTCAAT TTTTCACTAG AATAATAAGC TAGTATAGTA AACTGAAATA    3480

AGATATAAAC AAATAAATTG GAGCTTAACA TCCATTTCCA GCAATTTTTT AGAAACTACA    3540

GTGGACTATT CTAGATTCAA CATATTATAA AAACTAGAGT AAAAGAAAAG GATTGGATCT    3600

TGTGTAATGC AGGATCCAAT CCTTTCAATC ATTTTGTCCA ACTTTTGGAG GTTCCTACAA    3660

TGTAGTCGTC ATTAATAAAG ACAGATGGGA ATGACAGTGT TCCTATTTAT TTTGATAGAG    3720

ATCGATGAAT TCTTTAGATA GCAACTGAAT AATCTCTGTT GAAGCCATTT GGTCTTCTGC    3780

ATGCATAAAT AGCAAGGAGA ATCCTATTTT TTCTCCAGTA GCTTCTTTTT GTATGAGATT    3840

AGAGTGAATC TTGTGCGCTT CTACTAAGGA GTCTTCCGCT TCTTCAACTT TAATTTTCGC    3900

TTCTTTTAAA TTTCCTGCCT TAGCTAGTTG GATGGCTTCA ATAAAGGATG ATTTGGCTGC    3960

TCCACTATTG GCAATGAGCT GAAAACAGAT ATATTCCATT TCTTCTGTCA TCTTATTTCT    4020

CCTATCCATG CAAGTGCTTG TTCCAGAACT TTTGCTCCAT TCATCATTCC GTAATCCCGC    4080

ATATCAATGG TATCTACAGG GATATTTCCT GCAATTTCTT TCACAGCAAG TAACTCATAA    4140

CGAATTTGTG GCCCAATTAG AATGACATCT GCTTCATGGA TATTCTTTTT AGCTTCTGTC    4200

ATTGATTTTG CTTGGATAGA GATTTCAATC CCACGTTCAG TCGCACTTTG TTGCATTTTT    4260

TTAACAAGCA TACTTGTCGA CATTCCCGCA TTACATACTA ATAAAATTTG TTTCATAATC    4320

TTAACCTTCC ATTTCTTGTT CAACAACTTT GTCATTAACT TTGATAAATG GAATGTATAG    4380

AAGAACTCCA AGTGCAAAGA TGATGAATTG AACTAGAACT GCTCTCACGT CCCCTGCTGT    4440

TGCTAACCAT GCATTTAAGA ATACTGGTGT AGTCCAAGGA ACTTGTATAA ATGCAGGACT    4500

CATGAATTCT GTAACTGTTG CTAAGTAGCT GATTAAAATA CCAAGGACTG GAACTGTGAT    4560
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1225

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AAATGGAATA GCTAATGAAA TGTTATAAAC GATTGGGTAA CCGAATAATA CTGGTTCATT        4620

GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTTTAGAGA CAGCATTGCG        4680

ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCAC CCATTAAAGC        4740

GAATGTTTGT ATTTGTGATA GGTTGATGAT GTGTGGAATG GCTTGTCCAT TATTTGCTGC        4800

AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTTCT AGGATGGCAC TGTAAATAAC        4860

TGCTTGGTGA ATACCAAATA GCCATAACAT ATTTCCTAAA GAGTAAATAA TAATGACCCC        4920

GATTAAGCTT GTACCAATAT GACGAATTGG TTCTTGAATA AAGATTGTAA TGATTGAGAT        4980

TAAGTTCATT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC        5040

GGTCATGACT GGAAGTAATA CGCTAAATGA TCTACTAACA GCTGGTGGAA TATTTTCACC        5100

AAGGTTCATT TGTAAAGCTT TAACGTTTGA TAATTCAATG AATAATTCTG TTGCAATAAT        5160

CGtACGATAA CCCCGGCGAA CATTGCGCCT GTACCTGTGT TGTTGAATGA AAGAACACCT        5220

GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAACTACAG AAACTGTATT TGGCATCATC        5280

ACAATTAAAG AAACTAATGA TAGCATTGAT GCTGCTAACG GGTTTTCGAA ATCTCTGTTT        5340

TTAGCTAAGA AATAACCAAC CATTACAGCA ATAATCATAC CTGAAATACT TAAAGTACCG        5400

TTTGCAATTG TTATTCCCCA ATATTGGAAT CTTGTTAATG TATCCCCTTG GAAAATCCAC        5460

TTAAATACCG TGTTGTTCAA AAGAACGATT AAACCTGCCA AAATATATAA TGGCATTACT        5520

GTTACGAATG CATCTCTTAG GGTTTTTAAA TGAATTTGGT TCCCTAGTTT ACCAGCAAAG        5580

GATGGCAAAA AAATTTTTTT GGGGGGGGGG GTTATTAAAC CCCCCTTTTT AAAAAAAA        5638
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(2) INFORMATION FOR SEQ ID NO: 218:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4745 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

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CCGGAAGCTG TTGCCCTTGG AACTCCAAAT GAAGAAACAG CCTTTGTCTT GAACTATTTT         60

GGTGTGGAAG CACCACGTGT TATCACTTCT GCCAAAGCAG AGGGGGCAGA GCAAGTTATC        120

TTGACTGACC ACAATGAATT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC        180

GGTGTTGTAG ACCACCACCG TGTGGCTAAC TTTGAAACTG CAAGCCCACT TTACATGCGT        240

TTGGAGCCAG TTGGATCAGC GTCTTCAATC GTTTACCGTA TGTTCAAAGA ACATGGTGTA        300
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1226

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GCTGTGCCTA AAGAGATTGC AGGTTTGATG CTTTCAGGTT TGATTTCAGA TACCCTTCTT      360

TTGAAATCAC CAACAACACA CCCAACAGAT AAAATCATTG CTCCTGAATT GGCTGAATTG      420

GCTGGTGTGA ACTTGGAAGA ATATGGTTTG GCAATGTTGA AAGCTGGTAC CAACTTGGCT      480

AGCAAATCTG CTGAAGAATT GATTGATATC GATGCTAAGA CTTTTGAACT CAACGGAAAT      540

AATGTCCGTG TTGCCCAAGT GAACACAGTT GACATCGCTG AAGTTTTGGA ACGCCAAGCA      600

GAAATTGAAG CTGCAATGCA AGCTGCCAAC GAATCAAACG GCTACTCTGA CTTTGTCTTG      660

ATGATTACAG ATATCGTCAA CTCAAACTCA GAAATCTTGG CTCTTGGTGC CAATATGGAC      720

AAGGTCGAAG CGGCTTTCAA CTTCAAACTT GAAAACAATC ATGCCTTCCT TGCTGGTGCC      780

GTTTCACGTA AGAAACAAGT GGTACCTCAA TTGACTGAAA GCTTTAATGC GTAAGATTTT      840

GGGTGTCAGC TCAAAATCGG AAAGTCTAGT TTGCCTTATA TCGCAAGGAG TTTCGGCTCC      900

TTTTTTCTAG GAGTGAAGTA TGTTAGAAAA TGGCGATTTG ATTTTTGTGA GAGATGGGTC      960

AGACATGGGA CAGGCCATCC AGACTTCCAC AGGTAACTAT AGCCATGTTG CCATTTATTT     1020

GGATGGGATG ATTTATCATG CTAGTGGACA GGCTGGTGTT GTCTGTCAAG AACCGGCAGA     1080

CTTCTTTGAG TCCAATCATT TATACGACCT CTATGTTTAC CCAGAAATGG ATATCCAGTC     1140

GGTGAAGGAA AGAGCTTGCA AACATCTTGG AGCACCCTAC AATGCTTCTT TCTATCCAGA     1200

TGCAGCTGGT TTTTACTGCT CCCAGTATAT AGCAGAAATC CTACCTATTT TTGAAACTAT     1260

TCCTATGAAA TTTGGAGwTG GGGAGCAGGA GATTAGTGAT TTTTGGAGGG AGTATTACAT     1320

AGAACTAGGT CTGCCTGTTC CTCTGAACCA AGCTGGTACC AATCCTAGTC AGTTGGCAGC     1380

ATCGCCTCTG TTACAATGTA AAGAAAGGAA TCTTCATGAT TCAGATTTTT AATCCATCTC     1440

GTTTGACGAG ACAGCCATTT TTGGAGAATT GATCCGCTAT CTGGATCAGT ATGAGGATGT     1500

GATTCTACGG GAAATTAAGG CTCAATTTCC AGATGTTGCA GTTGATAAAC TCATGGAAGA     1560

GTATATAAAG GCAGGCTTGA TTCTACGTGA AAATAAGCGC TATTACCTCA ATTTTCCTAC     1620

GCTTGAATCA CTTGATAGTC TTGAACTGGA TCAAGAGATT TTTGTCAGAG AAGCTAGTCC     1680

GGTCTATCAA GCCTTGTTGG AGCAGAGTTT TGAGACGGAA TTGCGCAATC AAATCAATGC     1740

AGCTATTTTA GTTGAAAAGA CGGACTTTGC GCGCATTAAA ATGACCCTGT CCAATTATTT     1800

TTACAAGGTC AAACAGCAGT ATCCTTTGAC AGAAAAACAG CAGGAGCTCT ATGACATTTT     1860

AGGAGATGTT AATCCTGAGT ATGCCCTCAA GTATATGACG GCTTTTTTGT TGAAATTTCT     1920

CAAAAAAGAC CAGCTTATGC AGAAATGCCG TGATATCTTT GTGGACAGTT AGGTTGTCTT     1980

AGGCTATATT GTGCAAAATG AAGATGGAAA GTATGAGTTG GCTATCGATT TTGATAAGGA     2040

GAGGTTAACT TTCTACTTAG CGTGATTTCT TGTTTCTGAG TACATTGTTT GACTTTCCTT     2100
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1227

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AGTATTCGGT ATAAACTATA TGTAACCGGT AACACATATC GGAATAAACT AAAGGAGACA     2160

ATCATATGTC ACTTGAAAAC AAATTGGAAC AAGCAACAGG CGCTGTCAAA GAAGGTTTTG     2220

GTAAAGTTAC TGGAGACAGC AAGACAGAAC TTGAAGGAGC TGTTGAAAAA ACAGTTGCTA     2280

AGGCAAAAGA CGTTGTAGAA GACGCAAAAG GTGCTGTAGA AGGTGCCGTT GAAGGTTTGA     2340

AAAACGTTTT TACTAAAGAA TAGGAAAAAA TCAAGGGTTT CATTTTCCCT TGATTTTTTC     2400

TATTCTTATA AATAATTTTC TGCGACGGCT GTATCTCCTG GGTAGGATTC TTTCTTGCCC     2460

TGGATGATTT GGTAACAATC GGCTCCCTTA CCCGCAATAA TAACTGCATC TAATTCGTGA     2520

TTTGTGATAG CCATTGCCGC CTTGATGGCT TCTTGGCGAT CCGCAATCTT TTCAACAGGA     2580

TGATTGATGT AGCTACTAAT TTCATCTGCA ATGGCCATTG GGTCTTCATA GTTAGGGTCA     2640

TCAGCAGTCA GAAAGACTTG AATCTCAGGG TGTTGATTGA GGAGGAGGCC AAAGTCCTTA     2700

CGACGACTTT CTCCCTTGTT TCCTGTTGAT CCCAGAACCA GAGCAATCTT TCCGTTTGA      2760

TGAGTTTCAA CCACATTGAT GAGTTTTTTC AGACTATCCC CATTGTGGGC ATAGTCGATG     2820

AAGACCTTGG CTCCATTTTT CTGAGTGAGG ACTTCCATAC GACCAGGAAC GCGGGTTGCA     2880

GCGATGCCTT TTTTGATGTC CTCAAGACTT GCTCCGAGAC GGAGACAAGC AAGTCCAGCA     2940

GCAACTGCAT TTTCTTGGTT GAAGTTGCCA ATGAGTTGAA TATCATAATC TCCAGCGAGT     3000

TTACCCGTAG CTGAAAAGCT AAAGGCTTTG GAATTCTCGA TTTGGTTATC AAATTGGCTA     3060

CCATAGAAAT CATGGTCTTG ATCTTCAACC TGTTCTTTCA AGACTGAGAA GTGGTCCATG     3120

TCACTGTTAA TGATGACTGC TCGGCTCTTT TCCATCAAGA GACGCTTGTG GTAGAAATAG     3180

TCTTCAAAGC TAGGGTGTTC AATCGGGCCG ATATGGTCTG GGCTGATATT TAGGAAAACT     3240

CCCACATCAA AGGTTAGACC ATAGACACGT TTGACCAGAT AGGCTTGACT GGAGACTTCC     3300

ATGATGAGGT GGGTACGGTC ATTTTGCACA GCCTGATTCA TCATGTCAAA GAGGTCAATA     3360

CTCTCAGGGG TTGTCAACGC TGACTTAAAG AAAGTCTCGC CATCAAGAGT TGTGTTCATG     3420

GTCGACAACA TAGCAGGTCT ATGCCCTTGA GATAAGATGT TATAGGCGAA ATAGGCTGCT     3480

GTTGTCTTAC CCTTAGTACC AGTAAAGGCA AGGAGTTTGA GTTTTTCCTG TGGATTACCA     3540

TAGAACTCCA TGGCAATCAA ACTCATGGCT TTCTTTATAT CGTTCACAAT GATGACAGGG     3600

ATACCGACTT CGTAGTCCTT TTCAGCTACA TACCAAGCTA ATCCTTGTGT TATAGCAGAA     3660

AGAAGGTATT CTTTTTTAAA GGCAGCGCCT TTTGCGAAAA AAAGAGTGTC TTCTGTTACT     3720

TTTCGGCTGT CGTAGCTGAT GCTATCAAAA ATAACTTTGC TGTAGTTGTA GTGGTAATGA     3780

CCTTGGTCAA TAATTTCGCG AAAAAGGCCA TCTTTCTTTA AAATATCTAA TACGGTTTCA     3840
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                                    1228
     ATCTTAATCA TACTTTCTAT TGTAAACCGA AAGTCGTAAA TTTACAAGTA ACAAGGAAAA    3900

     GTTTATAATG GAAGATAAGG AGTTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT    3960

     CGCACGAAAA CAATCACCAG CAGGCCCAGA TGTTACGGGG GACTGCTTGG CTAACGGCTA    4020

     GTAACTTTAT CAGTCGCCTA CTCGGGGCTG TTTACATTAT CCCTTGGTAC ATCTGGATGG    4080

     GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAATATC TATGCTTGGT    4140

     TCTTGTTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAGCAAGTT GCCAAGTATA    4200

     ATACCATGCG AGAAGAAGAG CATAGCTTTG CCCTGATTCG GAGCTTCTTA GGCTTTATGA    4260

     CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGTATGTCTT TGCTCCTTGG CTAGCAGACT    4320

     TGTCTGGCGT GGGCAAAGAC TTGATCCCAA TCATGCAAAG CTTGGCTTGG GGAGTCTTGA    4380

     TTTTCCCGTC TATGAGTGTT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCCT    4440

     ATGCCATGAG CCAAATTGCT GAGCAGGTCA TTCGTGTTAT CTGGATGCTC CTAGCAACCT    4500

     TTATCATTAT GAAGCTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAACCTTTG    4560

     CTGCCTTTGT CGGTATGGTA GCCAGTTTTG CAGTCTTGAT TTATTTCCTT GCCCAAGAAG    4620

     GTTCACTCAA AAGAATCTTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGGTTG    4680

     ATACCATTAA GGAAGCCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCCAGA    4740

     TTTTG                                                                4745
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(2) INFORMATION FOR SEQ ID NO: 219:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1900 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

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     CCTGATTGAC CTTATAATAA GGAACAAAAC ACAATGCACT ACCTTTTCAA CAAAAGAGTT      60

     GCTGCTTGAT TAAAACCATC ACACCAGTTA TACCATTTTG CTTCATACCC ATCTTGAGCT     120

     AGGATACGAT CTTCTAAATC AAAAACAGAG TAAATCTTTC TTTCCTCGCA AGCTTGCGCA     180

     TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCACT CAGCAGAAAT CGTATCCCGA     240

     CCTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA     300

     AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA     360

     ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATATTG     420

     ACTTTCATTT CTTTCTCCTC AAGGGAATTC GATACTCACT TCTGTTTGCC TTTAAATCGC     480
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1229

CATTGGAAGC GGAgCTTGTC ATAAAAGGGA AACTCGATAA ACAGGACTCC CAAGCCCACA   540

CAGAGACTGG CAAGGACGTC TGATGGGTAA TGAACTCCCA GATAGACTCT TGATACCAGC   600

ACACTGACTA GGTAGAGGCC AAGGACGATT TGTACGATTT TTCTCCAGAC CTGATCTTTA   660

ATCCGCTGAC TAAGAATAAC AATCAAAGTC CCTACCATCA GCGTTACAGC TAGAGAATGC   720

CCACTTGGGA AGGAAAATCC CTTCTCCTCC ACCAGATGTA AAATAGCTGG TCGTGGGCGC   780

TGGTAGATAT TTTTAAAGGT CACGATTAAA AGACCTGCCA AAGCCAGATT TCCCAGCATG   840

AAGAAACTTT CTATCTTCCA TCGCTTACGA TAAAAGACAA AAGCTGTAAT GACAACCCAA   900

GTGATAATCA CTGGGATATC AATCAGACGT GTGAGGGCTC GAAAAAGAAT AGTCAAATAA   960

TCTGGTAAGT CTCCTCGAAT GGCAGTCTGA ATCGATTGGT CAAAATTGAC CAACATTTCA   1020

GGGTAAAATT TGACCATGTA GCCAAGAATA ACGAAAAGTA AAAGGGCAAA ACTGCCCTTC   1080

ATTAAAAATG TTTGTTTATC TCTCATAATG TTTTAAGGTT GGTTTCAAGA GAACATACAA   1140

CAACCAGAAT GAAACGGAAA AGATAACACC TTCAATCAAG TTAAAAGGTA ATACCATGGT   1200

CATTAGGTAG TTGGAAAGTC CCAAAATTTT TCCAATATCA AAGTTAGCAA ACTTAGCGTA   1260

CAAAGGAACA GCATAAACAT AGTTGAGAAC CAACATGGCC AAGGTTAAAC CAATAGTTCC   1320

AGCTAGAGAG CCTAGTAGGA AACGAAGGGT TGTCCGTTCC TTTTTCCAAA TCAAAGCAAA   1380

TACGATGACA AAAACTCCCA AAGCTACGAT ATTCATCGGC AAACCAATGT AAGTATTCAC   1440

TCCTTGGCTG TTAAGAAGCA ATTTCAAGAG TGAGCGAAGC AAGAGCACTC CTAGAGmCsC   1500

AGGCAAATCC ATGACCACCA GACCCACAAG GACTGGCAAG ATACTAAATT CGATCTTGAG   1560

GAAAGATGCC GCTGGTAAAA GCGGAAAGTC AAAGTACATC AGCACAAATG AGATGGCTGA   1620

TAGAATTGCA ATGGTCGAAA GTCGACGTGT GTTTGTCATA ACAGGTTCCT CCAATTTTCT   1680

ATAAAATCAG AAGAAGTTGG AAAGGATTCC TCTATCTATT CTCACTTTTT ATATCCCAAA   1740

AGTTCCCTCT TACTCTATTA AAGAAAAACA AAGCAAGTGG TTACAATCCG GCTATAAATC   1800

TATCAAAACA GACAAGGCTA TTCTTTCGTC TTCTCCCATC CAGACTATAC TGTCGGTTGT   1860

GGAATCTCAC CACATCACGT TGCGCTCACG GACTTCTTTA   1900

(2) INFORMATION FOR SEQ ID NO: 220:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 4692 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

1230
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

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GGTTTTCCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCCATCTGCT CACGATAGAT        60

GAATAATGAT ATTTTTTACC ATGATAGTAA TTTGAAAAAG CCTAACCACC TCCTGAACCT       120

TCTCCATATG TCCATACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT       180

AATGTAAAAC TTGAAATAAG AGCTAGAGCA AGTAATCTAT GTTTTTTCGT TTTCATTTTA       240

TTTTTTCTTT CAAAAAAAGC ACACCTTGAG CAACAATGCA ACAAAATAAA TCCTCCTCTC       300

TCTTTTATTG AAACCGCTTT CTTATGTGAT AAGAATAACT TTTTTATtAT TTGTTGTCAA       360

GGAAAAAATC GAATTTTTTA GATATTTTAC TATATTACCT CTGTGAATAA TATTATATAG       420

TAGTTTTATT TCAAAATAAT ATGCAACCAG TACTAACCAA ATATAAAATA GATGCCATTA       480

ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTTAACT       540

AAAAAGCAAT TCAAACTATT GTAAAATTCC TAGCAAAAAG AGAGCCGAAA CTCTCTTTTT       600

TATCTTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACACT AAAGTAAGCT       660

AGGATCAACA TGGCTATTGC TAGGAATATT TCTGTTGGTA ATTGAAAAAT TTTCAGAAAA       720

GATAGAACCA ATAAAATCAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA       780

GTCCCTTTAA TGCTTTCTGG TGTCGCAAAT ACATAGAGTA GGAGCAGTAA AATTCCTAGG       840

ACTAAATAGA CCATCTTTCT CTCTTTCTAG CTCTTATTCA GCTGATTTTT TCTTCTTGTT       900

AGCTTTCTCA CGCTCTGCTT TGTTAAGGAT TTGTTTACGC AAACGGATAG ACTCAGGCGT       960

TACTTCCATG TACTCATCGT CGTTCAAGAA CTCAAGAGAC TCTTCAAGTG TCAAGATACG      1020

AGGCGTCTTG ATAACAGCTG TTTGGTCCTT AGTAGCTGAA CGAACGTTGG TCATTTGTTT      1080

TGCCTTCGTG ATGTTAACTG TCAAGTCATT TTCACGAGAG TTTTCACCGA TGATCATTCC      1140

TTCATAAACC TCAGTACCTG GGTTGACAAA GATCGTACCA CGTTCTTCGA TAGACATGAT      1200

TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAGG GCACCACGGT GACGTCCACC      1260

AATTTCCCCT GGAATCAATG GCAAGTATTG GTCGAAGGTA TGGTTCATGA TACCGTAACC      1320

ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAATCAAA CCACGCGCTG GAACAAGGAA      1380

GACCAAACGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTCAC CTTTACGTTC      1440

AGAAAGGCTT TGGATAACAG ACCCTTGGTA TTCTTCTGGA GTGTCGATTT GTACACGTTC      1500

AAATGGTTCA CATTTAATAC CGTCGATTTC TTTTACGATA ACTTCTGGAC GAGATACTTG      1560

AAGTTCATAG CCCTCACGAC GCATTGTTTC GATAAGGATT GACAAGTGCA ATTCTCCACG      1620

TCCTGAAACA GTCCATTTAT CTGGTGAATC AGTTGGGTCA ACACGAAGGG AAACGTCTGT      1680

TTGCAATTCT GCCTGCAAGC GTTCTTCCAC CTTACGAGAA GTTACCCATT TACCTTCTTT      1740
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1231

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ACCAGCAAAT GGTGAGTTGT TGACCAAGAA AGTCATTTGA AGAGTTGGCT CATCGATGTG        1800

TAGGATTGGA AGAGCTTCTA CTGCATCTGT CGGAGTGATG GTTTCACCGA CAAAGATGTC        1860

TTCCATACCT GAAACGGCAA TCAAGTCACC CGCTTTGGCT TCTTGGATTT CACGACGTTC        1920

CAAACCAAAG AAACCGAAGA GTTTTGTAAC ACGGAAGTTT TTAGTTGTAC CGTCAAGTTT        1980

AGAAAGGGTA ACTTGGTCCC CAACCTTAAC TGTACCACGG AAGACACGAC CGATACCGAT        2040

ACGTCCAACG AAGTCATTGT AGTCCAAAAG TGACACTTGG AACTGCAAAG GCTCATCTGA        2100

GTTATCTACT GGAGCTGGGA TATGGTCGAT AATCGTGTCA AAGATTGGTG CCATAGTCGC        2160

TTCTTGGTCA GCTGGATCAT CTGACAATGA AGAAGTTCCG TTGATCGCTG AAGCATAAAC        2220

CACTGGGAAA TCAAGCTGGT CGTCATCTGC ACCAAGCTCG ATGAAAAGTT CCAAGACTTC        2280

ATCCACTACT TCTGCTGGAC GAGCTGATGG CTTATCGATT TTGTTAACAA CCACGATTGG        2340

GACAAGGTCT TGTTCCAAGG CTTTTTTCAA TACGAAACGA GTTTGTGGCA TGGTTCCTTC        2400

ATAGGCATCT ACGACCAAGA CAACACCGTC AACCATTTTC ATGATACGCT CAACTTCTCC        2460

ACCAAAGTCC GCGTGTCCTG GTGTGTCCAT AATGTTGATA CGAGTTCCGT TGTAAGCAAC        2520

GGCAGTATTT TTAGCAAGGA TGGTAATTCC ACGCTCTTTT TCGATATCGT TTGAGTCCAT        2580

AGCACGCTCT GCCAATTCAG TCCGTGCATC AAGCGTTTCT GATTGTTTCA ATAATTCGTC        2640

AACCAGGGTT GTTTTACCGT GGTCAACGTG GGCGATAATC GCAATGTTAC GGATATCTTC        2700

TCTTAATTTT GTCATGATTT CCTCTATAAT ATTCAAAATT TATTTTCTAA CTGAACGATT        2760

ATACCATAAT TTCAAATAAA TAACATAACT CAAGCAAGTG TAAATGTTTT CACTCTGCTT        2820

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CAGGACTACA AGAACTCCTT TTTCAGGATC GAATCATTCA AGGCTATGAA CACACCTATC        3060

TTATGCTTCA TAAACCTGCT GGTGCCGTTA CAGCCAACAA AGACAAGGAA CTTCCGACCG        3120

TCATGGACCT GCTTCCATCT AACATCCAGT CTGACAAGCT CTATGCCGTT GGCCGACTGG        3180

ACCGAGATAC AACGGGACTC CTCCTCTTGA CCGATAACGG TCCCTTGGGC TTTCAGCTCC        3240

TCCATCCCCA ATATCATGTC GATAAGACTT ACCAAGTTGA GGTTAATGGA CTTCTAACAC        3300

CTGACCATAT CCAAACCTTT CAAAAAGGAA TTGTCTTTTT AGATGACACT GTCTGTAAAC        3360

CCGCAAAACT AGAGATTCTA TCTGCAAGTC sCTCCCTCAG TCAAGCCTCT ATCACCATTT        3420

CAGAAGGAAA ATTTCATCAA ATCAAGAAAA TGTTCCTCTC GGTTGGTGTT AAGGTGACTA        3480
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1232

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GCCTCAAAAG AATCCAATTT GGGGACTTCA CATTGAACCC AGATTTAGCA GAAGGTAACT    3540

ACCGCCCTTT GAACCAAAAA GAGTTACAAA TCATTAAAAA CTATTTAGAG ATGAGTCGAT    3600

AAAACAAAAA AAGCTTTAAA ACTAAAGCTT TTTTCTTTTA TTTACCGAAA AATTAAGGCG    3660

ATTGCTACAA TCCAGTTAAC TACAGAAATC ACAATTCCTA AGATATTAAG AATCTTTTCT    3720

ATTTTATAGT CTAATTGTGA CTCTTTTTGG TATGAAATAG CCAAGACCAA TCCTATGATA    3780

CCCAAAATCA GGCCTACAAT TGGAAATAAC AAACCAAGAA TAATCGACAA GATACCCACA    3840

AAAAGTGGAT TTTTCTTCTT TTCTTTTATG TTCTAAGAAC TCCTTAAATT TTATACAAAT    3900

TAATTATACT ATAAAACAAT AGCTTCATCC TATCATTCGA CTAATTTGGA AATAAGGTTA    3960

GCTAGTCTTC ACTTTCCCTT TCCAAGAATC CAAGCCATAA GAAAGGATAT AAATCTCAGA    4020

AAAACCTTGT TTTTTCAAGT AAAGAGCTGC ATTTGTAACT CGTTGCGCAC GTTGGTTTTC    4080

GTAGAGAAGG ACAGGTTTAT CTTTACGAAG GGCTGCAAGA CTAGTTTTCA ACTGACTTGA    4140

AGGAATATTG CGTGCACCAA GGATATGTTT TCTGTGGAAT TCTGCTGGGT CGCGCAAATC    4200

AATCAATTGA CCCGTACGAA TCAAGGCTTC AAACTCCTCA TTGTCCACAA TTTTAGCCGC    4260

ACGGCGAATA CGAAGATAGT TAAAGCCCAT CCACGCCAAC ATTGCTAGTA TAAGTGCCCA    4320

CAAAATCCAA GTAACCATTA GTTCTTTTCT CCATTTTTCT CAATATAATC CAATTCTACC    4380

TTGTGCTCTC TGCGAAGAAC TGCTTCTGCC TCTAGATAGT CTAATTTATC CATCAACCCT    4440

GCATCGTAAA TCCGAGATAG TTCCAACTTC ATCAGTTCAA TATCATATAA GCGTTTTCCC    4500

ATGTAAACAA TAATACCAAA TCGTTTGAGG AATTGCTGCA CATCATAGAA TGTTTTCATA    4560

AGACTCATTC TAGCAAAATT TTGTGTTTTT TTCAAGAAGA GACTCACACA ATGCTCCTTA    4620

TTTTCCTATC TTCTTTAGCG ATTCTAAGGC AAGTATGGTA CAATAAAAAC ATGGGGATTC    4680

AACAATTACA TT                                                       4692
```

(2) INFORMATION FOR SEQ ID NO: 221:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 706 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```
GCTAAAAAGC TGATAATCTT CGACTCCTGT ATATGATGTG TCTTTTCATG TAAGACACGC    60

GCCGCCAGAA TCATGGCAAG AGCTGCAAGA CTGGCAAGTA AGAAGCCGAT AAGATAGGCA    120

AAAAGATAAG TGAATTTGAC AAAGAAAGTC AAAAGAACTA GGAAACCAAA GCCTCCTCCA    180
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1233

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AAAACTACCA AAGTCTTTCG TAAATCCCAG ATTTTATCCA ACTGCTTGAC GAGGGAAGTC        240

GTCTGACGAA CGCCTACAAT AGTTGCTAAC ATACTTCCTA AAAAGAATGG ATAGACATGA    .   300

GTTAAACTGG AGAAATAAAC AGAGGAATAA GAGGTCACTA GAAAACTACC AATAAACATG        360

GAGAAGAAAC TGATCAAGAA GGCAACAGCA GATAAGAGAA AGACCATCCC CTTCAACTGA        420

CCATTTGATT TAGCTTGTTT GGATAAGAAC CAAACTGCCA ATCCCCAAAG AATATAGTAG        480

TGAACCTCAA CTGCCAAACT CCAATTATGA ACAAACAAAT GAGGAATGAA CTGAGATTCA        540

TAACTCCCAC CTGTTAGGAG TTCATAGAAG TTGGTCATAA AGCCTAAGAC GCCCGCAATC        600

TGGCCACCAA TTCCAGCAAC ATAGTCTTGG CGAACCAAGA AAGTAAAAGG CATGGTCACC        660

AAGACCATCA AAACCACAGG TGGCACAATC TCGATAAAAG CGTCTT                      706
```

(2) INFORMATION FOR SEQ ID NO: 222:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 3236 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```
CAGCTGATGG GCAATATCAG TCATAGAAAT TTTTTCAATT AACTTTTGAG CAATTTTTTG         60

GTTGATGATA CGAGGGATTT GGTGATTTTT CTTTACCAGG GGAGTCTCAG CAACCATCAT        120

TTTTGAACAG TGATAGCACT TGAAACGGCG TTTTCTAAGG AGAATTCTAG AAGGCATACC        180

AGTTGTTTCG AGGTAAGGGA TCTTAGACGG TTTTTGAAAG TCATATTTCT TCATTAGACT        240

TCCACAATCA GGGCAAGATG GAGCCTCATA ATCCAGCTTA GCGATAATTT CTTTGTGGGT        300

ATCCATATTG ATGATATCTA GAATCTTGAT GTTTGGGTCT TTAATATCGA GCAGTTTTGT        360

GATAAAATGT AATTGTTCCA TATGATTCTT TCTAATGAGT TGTTTTGTCG CTTTTCATTA        420

TAGGTCATAT GGGACTTTTT TTCTACACAA AAATAAGCTC CATAATATCC ATAGGGGATT        480

TACCCACTAC AAATATTATA GAGCCCGAAA ATATGGGAAA ACTGATCCTT GTTTCTGCTT        540

TTGTCTATAG AAGAATAATA AAGATTATCT TCTTCAAATT CTCCGATATT CTCTAAAGTT    '   600

TTGTGCAAGT TGCACAGAAC TTGTTTATTT TTTTGGTCAT CTTGCCATAG AAATATAAAG        660

CGTTTTCATA TATAATATAA TTATCAAAAG ACAAAAGGAG TTCACCTCAT GGTAGAATTG        720

AATCTTAAAA ATATTTACAA AAAATATCCA AACAGCGAAC ACTATTCAGT TGAAGATTTC        780

AACTTGAACA TCAAAGATAA AGAATTTATC GTTTTCGTAG GACCTTCAGG ATGTGGTAAA        840
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                                    1234
TCAACTACAC TCCGTATGAT TGCTGGTCTT GAAGACATTA CAGAAGGTAC TGCATCTATC    900

GATGGCGTAG TTGTCAACGA CGTAGCTCCA AAAGACCGTG ATATCGCCAT GGTATTCCAA    960

AACTACGCTC TTTACCCACA CATGACTGTT TATGACAACA TGGCTTTCGG TTTGAAATTG   1020

CGTAAATACA GCAAAGAAGA CATTAACAAA CGTGTTCAAG AAGCAGCTGA AATACTTGGA   1080

TTGAAAGAAT TCTTGGAACG TAAACCAGCT GACCTTTCAG GTGGTCAACG TCAACGTGTT   1140

GCCATGGGGC GTGCGATTGT CCGTGATGCG AAAGTATTCT TGATGGACGA ACCTTTGTCA   1200

AACTTGGATG CCAAACTTCG TGTATCAATG CGTGCTGAAA TCGCTAAAAT TCACCGTCGT   1260

ATCGGAGCTA CAACTATCTA TGTAACTCAC GACCAAACAG AAGCGATGAC ACTTGCAGAC   1320

CGTATCGTTA TTATGTCAGC TACTAAGAAC CCTGCTGGTA CAGGTACTAT CGGACGTGTA   1380

GAACAAATCG GTACTCCTCA AGAAGTTTAC AAAAATCCAG TTAACAAATT CGTTGCAGGA   1440

TTCATCGGAA GCCCAGCTAT GAACTTCATC ACCGTGAAAT TGGTTGGTAG CGAAATTGTT   1500

TCTGACGGTT TCCGTTTGAA AGTGCCAGAA GGAGCATTGA AAGTTCTTCG TGAAAAAGGC   1560

TACGAAGGAA AAGAATTGAT CTTTGGTATC CGTCCAGAAG ACGTGAATGC AGAACCTGCT   1620

TTCCTTGAAA CATTCCCAGA CTGTGTTGTA AAAGCGACTA TCTCTGTATC AGAACTGCTT   1680

GGTTCAGAAT CTCACCTTTA CTGTCAAGTT GGTAAAGACG AGTTTGTTGC AAAAGTTGAT   1740

GCTCGTGACT ACTTGCAAAC AGGTGCAACA GTTGAGCTTG GATTTGACTT GAACAAAGCA   1800

CACTTCTTCG ATGTAGAAAC TGAAAAAACA ATCTACTAAA ATAAATAAAA TTCAAAGCAC   1860

TACAAGAAAA GATATCTCTT TATCAATTGT AGTGGAGAGA TATCAGTTAA TCTAGGGAGA   1920

GAAACAAAAT GCTTCTCTCC TTTTTGCTAG AGAAGTCATA TTATGCATCT ATATTGTGAT   1980

GCTCTTTAAT ACTCTTCGAA AATCTCTTCA AACCACGTCA ACGTCGCCTT GCCGTACGTA   2040

TGATTACTGA TTTCGTCAGT TTTATCTGCA ACCTCAAAGA TGTACTTTGA GCAGCTTACG   2100

GCTAGTTTCC TAGTTTGCTC TTTGATTTCC ATTGAGTATT ATTTGTGGGT ACCATCTACA   2160

AGTGAAGCTA TATGCGTAAA CTACGTGAGC AATTGAATTC GAACTAGAGA GGTAATAATA   2220

AATTTATGCT ATAGTTATGG TGACTTGTAT GCTTTTGATT CTAGTTTATC AAATAATAGA   2280

TTAGAATTGT CAGATAAATAT CATTTTGTGT TATAATGAAG AAAAAACAGA GGTGTTCAAA   2340

TGTCAGAAGC AGGTCATAAG TTTTTAGCAA AATTGGGGAA AAAACGCTTA CGTCCAGGTG   2400

GAAAGCGTGC CACAGATTGG TTAATTGCAG AAGGAGGATT TTCAAAAGAA AAGAGAATAC   2460

TAGAGGTTGC GTGTAATAGG GGAACTACAG CAATTGAGTT GGCACAGCGT TTTGGTTGCA   2520

AGATAACTGC TGTTGATATG GATGCTCAAG CTTTAGAAGT GGCTAAAAAA TCTGCTGGAA   2580

CGGCAGGTGT TGCTCATTTA ATCAGTTTTG AAAGAGCAAA TGCAATGAAA CTTCCTTATC   2640
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1235

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AAGATGCTAG TTTTGATATT GTTATAAATG AAGCTATGCT GACTATGCAA GCCGATCAAG    2700

CTAAGAAAAA ATGTGTAATG GAATATCTAA GGGTATTAAA ACCTGGAGGT CTTCTCTTGA    2760

CACATGATGT GCTTCTTAAG GAAGCTAAAG AGTCTATCAG ACAGGAATTA TCACAAGCAA    2820

TTCATGTAAA TGTAGGTCCT TTAACTCAAG ATGGTTGGGA ACAGGTGATG ATAGAATCAG    2880

GTTATTGTGA TGTGAAAGCA TTGACTGGTG AAATGACATT AATGAAATTA TCGGGTATGA    2940

TTTATGACGA AGGTTTGCTA GGAACTTTGA AAATTTGTGT AAATGCTTGT AAAAAGGAGA    3000

ATAGAAAGCA GTTTTTAACT ATGTATAAAA TGTTTGCTAA GAATAAACAG AAATTGGGCT    3060

TTATTGCGAT GGCTAGTTAT AAATCGTCAA AACGTTAGAT AATTATTGAA GTTAACTTTT    3120

CCTTTTTTCT TTCTTAAAAA ATATGCTATA ATAGAGAGTA AAAAACTTTG AAAGAAAGAA    3180

AAAGATGAAT TTAAAAGATT ACATTGCAAC AATTGAAAAT TATCCAAAGG GTACCG        3236
```

(2) INFORMATION FOR SEQ ID NO: 223:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2885 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```
CCTGACTTTT CAAATTGGTT AGTTTGCCAC ACTTGGTTTA TATGGTCGTG GAAAGCATGG    60

CTATTACTTC TCAAAGGGCG ATTTCTCACC CCATGAAAAG TGTCTATTTT TGTTTAGGTT    120

TGTAAGTTAA TTCATTGTCA CATATTACTC TTTAACTGAT TGAGTGAGTA CCGCTTATAT    180

TTGATGCCAA ACGCCTTAAA AGTGTTACCC TCAAGTCCTT TTAGAATACG GCTATAATTC    240

CGCTCATTGT AAACTATCTT AAGCTCATCA CTATCTAGGT TGGTATTAAA AATGGTATTT    300

TCACGATTGT TTAGCACGTC AAAGAGTAAA TCCTGCTCCC AGTCACTCTT AGGCTTAATA    360

ACAGCATTTT TTGCTCCTAA ATCATCAATA ATTAAGTAAT CAACAGACTT CATGAGTTCA    420

GTAGCTTCAA ACTCTGTAAG TGTTGCACCT TTACCATAAT TCCACCCCTC TTTAATTTGT    480

TTGATCATTT CGGTTAGGCT TACAAAAAGC ACACTCTTAG GTTCTCCTTT TGTCTTATAC    540

CCCTCATTTA TACCTTTGGC AATAGCAACT GATAAAAGTG TTTTTCCAAT CCCTGTACCT    600

CCTGTGATAA GCGTATTTCC CCTCATGCCA TCAAGATATT TTTGTACCTG ACCTTTTGCA    660

AATTCTAAAA ATCGCTTTTC TTCTGATGTT ACAGCATTAA AATCATCAAA AGTTTTAGTT    720

TTAAACTCAT CTGCTACATA GCTCTTATTG CTCATCAACA CATTATAAGT TTGCATATAT    780
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1236

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AGTTTAGCAT TCAAATTATC AGCAATCGCA TCTTCTTCAT CTTGCTTTTT CTGTTCTTCT      840

TGGCATTGTT CACAATAGGG TGGGATACAG CGAACTTCTT TTATTGCCTC TCCGTTCTCA      900

TTCCACCCCA CTACTACATG TCTTTCTCCT TTGATTTGTG TTAGCTGTAT TTCATGCTTA      960

GGACACAATT CGTCTAGTTT AAATGTCTCA ATATTTCCTA AACTAGATTG TAATGATTTC     1020

ATTTTCTGAC CTCCTAAAAT GGTTTTTCTT GTGTTGGTAT CCAATCTTCA TAGCTGGTAG     1080

GCTCTAGTTG ATTGGTTTGC TGTTTTTTAG CCTCACGCGC TGCCCTGCTA TTTCTAACAA     1140

GTTCCACCGT CAATAAATTG TCCTGTTTCC AACGGTTAAG GATTACCTTG ATGTATGCAA     1200

AGTTTGCTTT ACCCTGACTG ACAGCCTCTT TTAACGCCTC ATGGATAAGC TCTGGGCTAA     1260

AATCTTCTAG CATATACTGC AATTCTTGAA TCTGTAACGG TGACAATGCT TTACCTGTCT     1320

CAGCTCGCTT CATATTCAAC AAGTCGTCTA TTTCCACACT GGTTACTTTT TTATTTACAA     1380

AATCAGAAAT CAGTTGAAAA ATGTTTGGAC TTTGTAGCTG GATTTCAGCC ATTACCTCAT     1440

CAAATTCTGC TTGTGTCATG TTGTCTAAAT CTAGTGTCAT TGCATTGCCT CCTCAAACTT     1500

CTCTATAAGA CAACTTTTAT TTGCTTTCTG AGTTCCATTT TTAGAGTTAA AAAGAATATC     1560

TTTTAAGGTT ACAGTAGCCT CTAAATACTC CTTTTCAGCA TGCTCTATAT ACGCCTGTTG     1620

CTCTGCTTCG TTCTCAAAAA AGTGCTTAGC TTGGCGTTTA AAGAATGCTT TTCGCATAGC     1680

GTCCATTTCA AAAATACCAG GGGCGAAAAA CATTCCCGTA GTGCTTTTAG AGACCGCTTC     1740

GATTTTATGG CTTTCATTCA ATTCAGGAAG TTCAATCCAA AGTAAACGGG ACAACTCATC     1800

TTTGATGGAT TTTGTCTGAC TTTCCAATAA AGAAAGGATT CTTAGGCCAT TTTCTTCGCT     1860

AATTTCTCGC ATTTCTGCGC TAATTCTGTC TATACGTCTA GTTAAATTCT CATATGTTGT     1920

TTCTGTCATG TTTTTACCTC TGTTTCTTTG TTGGTGTGAT TTTTTAGCTT ATTTTTTTAC     1980

TTCTAAACAT CATTGTCTTA ATTTCCTGAT AACTCATTTT CAATTCAATC ATAGCTATTG     2040

CCATATCCTC AAATGCCTGG TACTGCTCCA ACTCCTCACT AGTCAAGCTA TCGATACCGT     2100

TATAGCCCCC ACGCTCTTCT CTTAACTGCT TAGCGTTCAT GTCTGTTACT GCCTTTAGTA     2160

GCAAGTTGTT CATGGTGCTA TGCGCGTGCT TTGGTGCATT AGGCCATGTT TCTATACTGT     2220

CATGCAAGGT TTTTCTTTTC GGTTTTTCTA GCGCCCTCTG CAGACGAATT TCAGAAAGTT     2280

CCTCACGCAT TTCAAAGAAT GCTTTGACTA GGTTTAGTTT GAATTGCCGT ACTGTTTCGG     2340

TATTCTTTAA ATAAGTGATC AGAAAAGTAG CCTGTTGCTC GTTCAGAATA TAGGATTTTT     2400

TAGGTTGTCC TCTAGTATCT AATTTATGGA TTTTAAATCC AAGTATTCCC AACTCTTCAA     2460

AGTCAGCCTT ATTTTCTCTT ATTAAGCGCG TGATAGTGTG GTGTTGTACT TCAGCACATT     2520

CAGCGATGAT CTCGCTTGTG GTGTACGGCT CTTTCTTACC GTCCATGTAA ACTAGTTCCA     2580
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1237

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TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTTAATTGCC TCCTCTAGCC     2640

TCTTTTTTAG CCTCTAAAAC GGCTTTGGCT AGTGGTTAAT ATTATTTACC ACTTGTCTCT     2700

ATAAACGTGT TAGAGGCCTT TATAACGACT TGTATCGCTG TATCGATATC CTCCGTGGAA     2760

TAGTAGATTT ATTTTCTAAT ATCATTCAAG ACTTGTTTAA CCCATTTCTT GAAAGAAATA     2820

AAATTACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA     2880

CTTGG                                                                 2885
```

(2) INFORMATION FOR SEQ ID NO: 224:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3144 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```
TATCAATCCT TTCCCATTAT AGGAGCAACA GAGTGGGAGT AGTCATCTAA GGACTAATTT      60

ATGTATTTTT ACGAGTCAGT ATCTTGGGAT ACTGGTTTTT ACTTTTCTAG ACTTTTTGAC     120

TACTTGTTAA AACTGGGATA ATTTTCGACT GTTTAACAGT TATTATGCAA AGTCTAAAAG     180

ATTAGAATTG TCAAAACAAT CCGTCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG     240

AGAAGGAAAA ATGTCAAACT TTTATATTGC AAATAGGAGA AATCATGACA AAAACATTAA     300

AACGTCCTGA GGTTTTATCA CCTGCAGGGA CTTTAGAAGA GCTAAAGGTA GCTGTTCAGT     360

ATGGAGCAGA TGCTGTCTTT ATCGGTGGTC AGGCCTATGG TCTTCGTAGC CGTGCGGGAA     420

ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAGTAT GGTGCCAAGG     480

TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATGA AGCTGGTGCT GGTGAGTGGT     540

TCCGTAAACT GCGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCCTTGATTA     600

TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA     660

CTAACTATGA AACCCTTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGCGC     720

GTGAGGTTTC AATGGAAGAA TTAGCTGAGA TCCGCAAACG TACAGATGTT GAAATTGAAG     780

CCTTTGTCCA TGGAGCTATG TGTATTTCAT ACTCTGGACG TTGTACTCTT TCAAACCACA     840

TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGTC ATGCCGTTGG AAATACGACC     900

TTTACGATAT GCCATTTGGG AAAGAACGTA AGAGTTTGCA GGGTGAGATT CCAGAAGAAT     960

TTTCAATGTC AGCCGTTGAy ATGTCTATGA TTGACCACAT TCcAGATATG ATTGAAAATG    1020
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1238

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GTGTGGACAG TCTAAAAATC GAAGGACGTA TGrAGTCTAT TCACTAyGTA TCAACAGTAA        1080

CCAACTGCTA CAAGGCGGCT GTGGATGCCT ATCTTGAAAG TCCTGAAAAG TTTGAAGCTA        1140

TCAAACAAGA CTTGGTGGAC GAGATGTGGA AGGTTGCCCA ACGTGAACTG GCTACAGGAT        1200

TTTACTATGG TACACCATCT GAAAATGAGC AGTTGTTTGG TGCTCGTCGT AAAATCCCTG        1260

AGTACAAGTT TGTCGCTGAA GTGGTTTCTT ATGATGATGC GGCACAAACA GCAACTATTC        1320

GTCAACGAAA CGTCATTAAC GAAGGGGACC AAGTTGAGTT TTATGGTCCA GGTTTCCGTC        1380

ATTTTGAAAC CTATATTGAA GATTTGCATG ATGCTAAAGG CAATAAAATC GACCGCGCTC        1440

CAAATCCAAT GGAACTATTG ACTATTAAAG TCCCACAACC TGTTCAATCA GGAGACATGG        1500

TTCGAGCTCT TAAAGAGGGG CTTATCAATC TTTATAAGGA AGATGGAACC AGCGTCACAG        1560

TTCGTGCTTA ATGTAGTTGT TTAGTTTTAA AAAACTATGC AAAGCTCCAT ATACAACACT        1620

TAAACGAGAT TAAAGAATGG CGAAATCCCT TGATGCGCAA GAGATTAGCT GTCTTTTTTA        1680

TTTTTTAAGT GATAAAGTCG GAGTTTAGGC ATCAAAGCCT ATCAAATTAA ACAAAGAAGC        1740

GATGTCTTAG ATATTTTGAA AAAAATTAAT AAGCAGAAAA CTCTCTATTA TTTTGTTGTA        1800

GAGAGTTTTT TGTTAATAAA ATTTCACAAA ATGACATTTA TATATTGCAT TAAGTTAGAT        1860

ATATGATATA ATATTGTTAA AAAGAGGCGC AACTTTTTAA AATTAATGAG AATCAAAGAG        1920

AAAACCAATA ATATTAATGG AGGAATAAAA AATGTAAGTA AGCATTATGG TCATTCAATC        1980

ATTCTCAAAG ATATAAATTT TGCACTTAAC AAGGGTGAAA TTGTTGGTCT AGCAGGGAGA        2040

AATGGAGTTG GTAAGAGTAC GTTGATGAAA ATTCTTGTTC AGAATAATCA ACCGACTTCA        2100

GGTAATATTA TAAGCAGTGA TAATGTTGGG TATTTAATCG AAGAACCAAA ATTATTTTTA        2160

TCTAAAACAG GTTTAGAGAA TTTAAAAATAT TTGTCAAATT TATATGGTGT TGACTACAAT        2220

CAAGAAAGAT TTAGATGTTT GATCCAAGAG TTAGATTTGA CTCAGTCTAT TAATAAAAAA        2280

GTAAAGACCT ATTCTTTGGG TACAAAACAA AAATTAGCTT TGCTTCTAAC TCTCGTTACG        2340

GAACCTGATA TATTGATTTT AGATGAACCG ACTAATGGTT TAGATATTGA ATCATCACAA        2400

ATAGTTTTAG CGGTTCTAAA AAAATTAGCT TTACATGAAA ATGTGGGAAT TTTAATATCG        2460

AGTCATAAAT TAGAAGACAT TGAAGAAATT TGTGAGAGAG TTCTTTTCTT GGAGAACGGG        2520

CTTTTGACAT TTCAAAAAGT AGGAAAAGAT AGTCATAATT TCTTGTTTGA GATAGCTTTT        2580

TCATCAGCTA CAGATAGAGA CATTTTCATT ACCAAACAAG AATTTTGGGA TATTGTTTAG        2640

GAAGAGGGAT TGAGAATTAC TATGTCTGGG AATATTCAAA ATAGTGAGCT TTTTAAATTT        2700

TTTAACGAAA ACTCTATTAA AGTAGTTGAT TTTGAAACTA AAAAAGAGAG GCTTAAAGAT        2760

ATTTACCTAA ATCGTTCAAA ATAAAGGAAG GTTATAATCA TGAAATTAAA TAAACAGAAG        2820
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1239

| AATCGGATGA TTTACGTCTT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT | 2880 |

GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAGTAAAT TGGGTATTCC AGGTGATTTA   2940

GGATTAAATT TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT   3000

CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATw TGGTATTTTA   3060

GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAAATACGA TGATGATGAA TACTAGTAAT   3120

GATTTGTTTA TCAAAGCAAT TGAA   3144

(2) INFORMATION FOR SEQ ID NO: 225:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3766 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTTAAGGA GAAAGAATCA TGAAAATCAA AAAATGGCTT GGTCTAGCAG   60

CCCTTGCTAC AGTCGCAGGT TTGGCTCTTG CAGCTTGCGG AAACTCAGAA AAGAAAGCAG   120

ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGGTTCTGAA GAAAAACGTT   180

GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC CTTGGAATTT ACAGAGTTCA   240

CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA AGTAGATTTG AACGCTTTCC   300

AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG   360

CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT GAATGGAAGT GCCAACAAGT   420

ACACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC TGTACCGAAT GACGCTACAA   480

ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG   540

GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAACTTG AAAATCACTG   600

AATTGGACGC TAGCCAAACA GCTCGTTCAT TGTCATCAGT TGACGCTGCC GTTGTAAACA   660

ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC ACTTTTCAAA GAACAAGCTG   720

ATGAAAACTC AAAACAATGG TACAACATCA TTGTTGCAAA AAAAGATTGG GAAACATCAC   780

CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG   840

TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG GTAATAAGAA ACAGGGAGGT   900

GGGAGAGAAA ATTCCACCTC TTGCTTTTGT ATAGAGTATA GATTGTAAAG AAGACTATTC   960

GTTCATAGAA AGGTAGAGAG AATATGGTTT TTCCTAGCGA ACAAGAACAG ATTGAAAAAT   1020

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                                        1240
TTGAAAAGGA TCATGTAGCC CAGCATTATT TTGAGGTTTT GCGTACCTTG ATTTCTAAGA      1080

AATCAGTCTT TGCCCAGCAG GTTGGACTCA AGGAAGTCGC AAATTATCTG GGTGAGATTT      1140

TCAAGCGTGT TGGAGCTGAA GTGGAGATTG ATGAGAGCTA TACAGCGCCC TTTGTCATGG      1200

CACATTTCAA GAGTTCGCGT CCAGATGCCA AGACCTTGAT TTTCTATAAC CACTATGACA      1260

CTGTGCCAGC GGATGGGGAT CAGGTCTGGA CAGAGGATCC kTTTACGCTT TCGGTCCGCA      1320

ATGGCTTCAT GTATGGGCGT GGGGTTGATG ACGACAAGGG TCATATCACA GCTCGCTTGA      1380

GTGCTTTGAG AAAATATATG CAGCACCATG ATGATTTACC TGTCAATATC AGCTTTATCA      1440

TGGAGGGAGC GGAGGAATCG GCTTCAACAG ACCTAGATAA GTATTTGGAA AAGCATGCAG      1500

ACAAACTCCG TGGGGCGGAT TTGTTGGTCT GGGAACAAGG GACCAAAAAT GCCTTGGAAC      1560

AGCTGGAAAT TTCTGGTGGC AATAAGGGGA TTGTGACCTT TGATGCCAAG GTAAAAAGCG      1620

CTGATGTGGA TATCCACTCG AGTTATGGTG GTGTTGTGGA ATCAGCTCCT TGGTATCTCC      1680

TCCAAGCCTT ACAGTCTCTT CGTGCTGCGG ATGGCCGTAT CTTGGTTGAA GGCTTGTACG      1740

AAGAAGTACA AGAGCCCAAT GAACGAGAAA TGGCCTTGCT AGAAACTTAT GGTCAACGAA      1800

ACCCAGAGGA AGTTAGTCGG ATTTATGGAT TGGAGTTGCC TCTCTTACAG GAGGAGCGGA      1860

TGGCCTTTCT AAAACGTTTC TTTTTCGATC CAGCGCTTAA TATCGAAGGA ATCCAGTCTG      1920

GTTATCAAGG TCAGGGTGTT AAGACTATTT TACCTGCAGA AGCCAGTGCC AAGCTAGAGG      1980

TTCGTCTGGT TCCGGGCCTA GAACCGCATG ATGTTCTGGA AAAAATTCGG AAACAGCTAG      2040

ACAAAAATGG CTTTGATAAG GTAGAATTAT ACTATACCTT GGGAGAGATG AGCTATCGAA      2100

GCGATATGAG CGCACCAGCC ATTCTCAATG TGATCGAGTT GGCCAAGAAA TTCTATCCAC      2160

AGGGCGTTTC AGTCTTGCCG ACGACAGCGG GGACAGGACC TATGCATACG GTCTTTGATG      2220

CCCTAGAGGT ACCAATGGTT GCATTCGGTC TAGGAAATGC CAATAGCCGA GACCACGGTG      2280

GAGATGAAAA TGTGCGAATC GCTGATTATT ACACCCATAT CGAATTAGTA GAGGAGCTGA      2340

TTAGAAGCTA TGAGTAGAGA TATTATCAAG TTAGATCAGA TCGATGTGAC TTTTCACCAA      2400

AAGAAGAGAA CCATCACAGC GGTTAAGGAT GTGACCATTC ACATCCAAGA AGGGGATATC      2460

TACGGAATCG TTGGATATTC TGGAGCAGGA AAATCAACCC TTGTACGGGT GATTAATCTC      2520

TTGCAAAAAC CATCTGCAGG GAAAATTACC ATTGACGACG ATGTGATTTT TGACGGCAAG      2580

GTGACCTTGA CGGCAGAGCA GTTGCGTCGT AAACGTCAAG ATATCGGAAT GATTTTCCAG      2640

CATTTTAACC TGATGAGCCA AAAGACAGCA GAGGAGAATG TAGCCTTTGC CCTTAAACAC      2700

TCTGAACTCA GCAAGGAAGA AAAGAAGGCT AAAGTAGCTA AGTTGTTGGA CTTGGTTGGT      2760

TTGGCAGATC GTGCTGAAAA CTACCCTTCA CAACTATCTG GAGGGCAAAA ACAGCGTGTG      2820
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1241

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GCAATTGCGC GTGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTTCT      2880

GCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAAGATTT GAACCAAAAA      2940

TTAGGCTTGA CTGTTGTCTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC      3000

CGTGTTGCAG TTATGCAGGA TGGGCATTTG ATTGAAGAGG GTAGTGTGCT TGAAATCTTC      3060

TCAAACCCTA AACAACCTTT GACTCAAGAC TTTATCTCAA CAGCTACAGG TATTGACGAA      3120

GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGAACACT TGTCTGAAAA CAGTCTCTTG      3180

GTGCAACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG      3240

CATTACCAAG TAATGGCTAA TATTCTCTAT GGGAATATCG AAATTCTCGA TGGTACTCCT      3300

GTTGGAGAAT TGGTGGTGGT TTTGTCAGGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA      3360

GCCATTCGTC AAGCAGGTGT ACAACTAAAA GTATTGAAGG GAGTACAGTA AGATGGAATC      3420

ATTGATTCAA ACCTATTTAC CAAATGTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG      3480

GGGAACGGCT ATCTACTTAA CTCTTTATAT GACAGTTCTT TCCTTCATTA TCGGAGGCTT      3540

CTTGGGGCTA GTGGCAGGTC TCTTTCTCGT CTTGACAGCG CCAGGTGGTG TCTTGGAGAA      3600

TAAAGTCGTA TTCTGGATTT TAGACAAAAT TACCTCAATT TTTCGTGCGG TTCCCTTTAT      3660

CATCCTCTTG GCAATCTTGT CACCACTTTC TCACTTGATT GTTAAAACAA GTATCGGGCC      3720

AAATGCAGCC CTTGTCCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG                     3766
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(2) INFORMATION FOR SEQ ID NO: 226:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2520 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

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TGTTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTCGTC GGGACAGGAG CTGTTGTTTT       60

TGGAAATGGT CTTGATGGCC TTGGTCACCT TGGAATCGCC TTTGCCTTTG GTTTGGCAAT      120

CGTGGTGGCA GCCTACTCAA TCGGAACTGT TTCAGGTGCT CACTTGAACC CGGCTGTTTC      180

GATTGCTATG TTTGTAAACA AACGTTTGTC ATCTTCAGAA CTTGTAAACT ACATCCTTGG      240

TCAGGTTGTT GGAGCTTTCA TCGCTTCTGG CGCTGTCTTC TTCCTCTTGG CTAACTCAGG      300

TATGTCAACT GCTAGTCTTG GTGAAAATGC CTTGGCAAAC GGTGTCACTG TCTTTGGTGG      360

TTTCTTGTTT GAAGTCATCG CAACTTTCTT GTTTGTATTG GTTATCATGA CTGTGACTTC      420
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                                        1242
     AGAAAGCAAG GGCAATGGCG CGATTGCTGG TTTGGTAATC GGTTTGTCAT TGATGGCGAT        480

     GATTCTTGTC GGATTGAAGA TTACTGGACT TTCAGTAAAC CCAGCTCGTA GCTTGGCACC        540

     AGCTGTCTTG GTAGGCGGCG CAsCCTTCAA CAAGTTTGGA TTTTCATCCT TGCACCAATC        600

     GCTGGTGGAG TTCTTGCAGC CCTTGTTGCA AAAAATTTCC TTGGAACAGA AGAATAATTG        660

     AAACTCAAAA AGCCTTGCTC CTCATCTTGA GGAACAGGGC TTTTTCGTAT GATACTCTTC        720

     GAAAATCTCT TCAAACCACG TCAGCTTCAT CTTGCCGTAG TATGGTTACT GACTTCGTCA        780

     GTTCTATCCA CAACCTCAAA ACAGTGTTTT GATCTGACTT CGTCAGTTCT ATCTGCAACC        840

     TCAAAACAGT GTTTTAAGCT GACTTCGTCA GTTCTATCTG CAACCTCAAA ACAGTGTTTT        900

     AAGCTGACTT CGTCAGTTCT ATCTGCAACC TCAAAACAGT GTTTTAAGCT GACTTCGTCA        960

     GTTCTATCTG CAACCTCAAA ACAGTGTTTT AAGCTGACTT CGTCAGTTCT ATCCACAACC       1020

     TCAAAACAGT GTTTTGATCT GACTTCGTCA GTTCTATCCA CAACCTCAAA ACAGTGTTTT       1080

     GATCTGACTT CGTCAGTTCT ATCCACAACC TCAAAACAGT GCTTTGAGCA ACcTGCGGCT       1140

     AACTTCCTAG TTTGCTCTTT GATTTTCATT GAGTATGACT TTAGCGGTTG TCAATTTTCT       1200

     CTGGATAAAG GTCGTGTTGG AAGAGGCGTT GTTCTGCCAA GCCCTCATAC TTAGTTCCTT       1260

     GCTTACCGTA GTTGTAGTAG GGGTCGATTG AAATGCCACC GCGCGGAGTG AATTTTCCCC       1320

     AGACTTCTAA ATAGCGAGGG TCTAGCAAGT TGACCAAGTC TTTCCCGATG GTGTTGATAC       1380

     AGTTTTCGTG GAAATCTCCG TGGTTTCGGT AGCTAAATAG ATATAGTTTG AGGGATTTTG       1440

     ACTCGACACA GAGCTTGTCA GGAATGTAGG AAATATGAAT CGTCGCAAAG TCTGGCTGAG       1500

     CAGTGATTTG TCCCAGCAGA GACATATCGA GGATATGGTG ACGAATGCCC TGTTCCTTAG       1560

     CGATTTCTCT AGTAATTTGA ATTTCGAGGT GATGACGTTG GCCGTAGGCA AAGGTGACAG       1620

     CTTCGACTGT TTCATAGTGT TGCATGACCC AGAAAAGGCA GGTTGTTGAA TCTTGACCAC       1680

     CACTAAAGAC GACCAAGGCT AATTGACGTT TCATAGTACT CCTTCCAAAA TGGGAAATGT       1740

     TCAGAGCACG CAAAAAGCTC CCATTAGGGA GCTAAAAAAT ACCAAATCGA GGTTTTTTTA       1800

     GCGATGGCAT ATCCCAAACA TCGTAATATT CTACTTATAT AGTAAAATGA AATAAGAACA       1860

     GGACAAATCG ATCAGGACAG TCAAATCGAT TTCTAACAAT GTTTTAGAAG TAGAGGTGTA       1920

     CTATTCTAGT TTCAATCTAC TATAGTCTAG CATATTTTTT GAAAAATGGC AAAGGGCAAG       1980

     AAAAAAGAGA CCAAAGAAAG TACTTGGTCT CTCGTTTGAT TAGCTCAATT CAGCAATGAT       2040

     GGCCTTGATT TGTTCTGCTG TGTGAACACC TGCAACTTGT TTGACAACTT GGCCGTCTTT       2100

     TTTGAAGAGA AGAGTTGGAA TAGACATGAT TCCAAAAGCA CGAGCTGTGT TTGGATTTTC       2160

     ATCAACGTCC ATTTTAACGA TTTTCAAGAC ATCTTCTGAA AGTTCTTCAG ACAATTTGTC       2220
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1243

CAAGATTGGA CCTTGCATAC GACATGGACC ACACCAAGTT GCCCAGAAGT CTACTAAGAC   2280

CAAACCGTCT TTTGTTTCTT GTTCGAATGT TGCATCTGTA ATTGCTTTTG CCATTGTATT   2340

TCTCCTTTTT TTAGTTATAT TGGCTTAAAT CTTGTTTCAT GAGATAGAAG AAGATATCTC   2400

CATAAGTCCC ATGGTAGTCC AAATTATGAC CCTTGTAAGT TAATTTTTGG ACAGGGTAGT   2460

AkkCTGCGAC GCCGATAAGG CAAGCTTGTT GCGAACGTTC AAAGTCTTCA TAAGACTCGG   2520

(2) INFORMATION FOR SEQ ID NO: 227:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 5278 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG ATTTTGTTTT CAAAAACAAC GAAGAAAAAG ACCATGTTGC TCTACTTGGA   60

AGAATTGGCT CCGAACGTGT TTATCGATAT ATTAATAAAA AATATTTAGA TTTACCGGAA   120

ACATTCGAAA ATTATAATGT TTTTGTACCA GAAGCTAATG GAAGTGGTGC CTTAGGTGAA   180

GTCTTATCAA CACCCCTAAT CGGGGAACCC CTAATCGGGC ATACAGATAC TTTTTTATCT   240

ATTGGTAATT TTAAAACAAA ATTTGAAGCC GATGCTTGTA TTAAATTTAT TAAAACTAAA   300

TTCGCTAGAG TATTATTAGG TGTTTTGAAA GTTACTCAGC ATAATTCACG CAAAACTTGG   360

TATTACGTCC CCCTCCAAGA CTTTACGGTC AATTCGGACA TTGATTGGAC ACAATCAGTG   420

ACTGATATTG ACCGCCAGCT TGATCAAAAA TATGACTTTT CCCCTGAAGA AATTGCCTTT   480

ATTGAGAATC ATGTAAGGGA GATGGATTAG AAAAGTATTT TTATTTGACA AATAGTGCTC   540

AATGATCTAA AATGACTATA TAGGATTAGG TCAGGAAGCA TACGATGCCC TGACCCTTTT   600

TGTACTTATG AGATGAGAAA GTCATTTGTT AGATAAATTG ACTCGTTAGC AAACGTTCAA   660

AAAAGGAAAA CTTATGCCAG TAGAAATTAA AACCACTAAA GAAATTCATC CTAAAATCTA   720

TGCCTACACC ACACCGACAG TAACCAGTAA TGAAGGCTGG ATTAAGATTG GGTATACAGA   780

ACGTGATGTC ACACAACGTA TCAAGGAGCA AACGCATACA GCTCATATAG CTACAGATGT   840

CTTATGGACT GGTGATGCAG CTTATACAGA AGAGCCTGAT AAGGGGAAAA CTTTCAAGGA   900

CCATGATTTC CACCATTTCC TTTCTTTCCA TGATGTAGAA CGTCGTCCCA AGACGGAATG   960

GTTCTATTTT AATGGAACTC CTGAAAAATC AAAAAATCTT TTTGATAAGT TTGTTCAGCA   1020

TGATTTGTCT GGTTATCAGC CTGGAAAAGG ACAGGACTAT ACTCTGCGAC AAGAGCAAGA   1080

1244

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AGAAGCAGTT GCTAAGACAT TAGCTTATTT CCAAGAACAT GCTGGAGGCA AGTTTCTCTG   1140

GAATGCCAAG CCACGCTTTG GTAAAACCTT GTCTACCTAT GACCTAGCTC GACGGATGGA   1200

AGCTGTCAAT GTCCTAATTG TAACAAACCG CCCTGCCATT GCTAACTCAT GGTATGATGA   1260

TTTTGAAACA TTCATAGCAG GTCAAACGAC TTACAAGTTT GTTTCTGAAT CAGATAGCCT   1320

TAAGAGTCGT CCAATCTTGT CACGACAAGA ATTTCTTGGT ATTTTAGCTG ACGATGTAAG   1380

ACAACTTGCT TTTATCAGTC TCCAAGACTT GAAAGGATCT GTTTATTTAG GTGGAGAGCA   1440

CGATAAACTC AAATGGGTAA CTGATCTGCA TTGGGACTTG TTGGTTATTG ACGAGGCTCA   1500

TGAAGGAGTT GATACCTTCA AGACTGACCA AGCCTTTAAT AAGATTCGAC GAAATTTTAC   1560

TCTGCATTTG TCAGGTACAT CATTTAAAGC ATTGGCTAAA GGAGATTTTA CAGAGGAACA   1620

AATCTACAAC TGGTCTTATG CTGATGAGCA GGCTGCTAAG TATTCGTGGT CTCTTGAGCA   1680

AGAAGAGGAA AATCCTTATG AAAGCTTGCC TCAGTTGAAT CTCTTTACCT ATCAAATGTC   1740

TCAGATGATT GGCGAAAAGT TAGAAAAAGG CGCTCAGATC GATGGTGAAA ATATTGACTA   1800

TGTTTTTGAC TTAAGTGAAT TTTTCGCTAC AGATGATAAA GGGAAATTTA TTCATGAGCA   1860

TGATGTCAGA AATTGGTTAG ATACTCTATC AAGCAATGAA AAATATCCAT TTTCAACCAA   1920

AGAACTCCGT AATGAACTCA AGCATACTTT TTGGCTTTTA GAACGTGTCG CTTCGGCCAA   1980

AGCATTAAAA GCCCTACTAG AAGAACACCC AATCTATGAA AACTATGACA TCGTTCTAGC   2040

TGCTGGTGAC GGACGTATGT CCGAAGAAGA CGATAAAGTC AAACTCAAAT CCTTGGACTT   2100

GGTTAGAAAA GCGATAGCAG AGAATGACAA AACCATTACC CTATCCGTTG GTCAGCTGAC   2160

GACAGGTGTC ACTATCCCTG AATGGACAGG TGTATTGATG TTATCAAATT TGAAATCACC   2220

AGCTCTTTAT ATGCAGGCCG CCTTCCGTGC TCAAAATCCT TACTCATGGA GCGATAACAA   2280

AGGAAATCAC TTTCGCAAAG AAAGAGCCTA TGTATTTGAC TTTGCGCCGG AAAGAACCTT   2340

GATTCTCTTT GATGAGTTTG CCAACAACTT ATTGCTTGTA ACTGCAGCTG GTAGAGGAAC   2400

TTCAGCTACA CGCGAAGAAA ATATTAGAGA ATTATTAAAC TTCTTTCCAA TTATTGCCGA   2460

AGACCGTGCT GGTAAGATGG TTGAAATTGA TGCAAAGGCA GTTCTAACCA CTCCTCGCCA   2520

GATAAAAGCT AGAGAAGTTC TTAAACGAGG TTTTATGTCC AATCTCTTAT TTGATAATAT   2580

TAGTGGTATT TTCCAAGCAA GTCAAACAGT TTTAGATATT TTAAATGAGC TGCCAGTTGA   2640

AAAGGAAGGG AAGGTACAAG ATAGTTCTGA TTTATTAGAT TTTTCAGATG TTACAGTCGA   2700

TGATGAGGGA AATGCAGTAG TAGACCATGA AATTGTAGTT AATCAGCAAA TGCGACTTTT   2760

TGGTGAAAAA GTTTATGGAC TTGGTGAATC TGTTGCTGAG TTAGTCACAA AAGATGAGGA   2820

ACGAACTCAA AAACAGCTGG TCAATGACTT GAGTAAGACC GTTTCTTCAG TGATTGTAGA   2880
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1245

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GGAATTGAAA GCAGATTATT CTCTAAAAAC AAGGGAAACT GAGCAAATTA AGAAACAAAT    2940

TACAGCAACA CTTGAGAATG AAATTCGAAA AAATGATATC GAAAGAAAAA TTTCTGAAGC    3000

TCATATCAAG CAAGAGTTGC AACAGCAGCT CAAAGAAGCA AATGATAAAG CGCAAAAAGA    3060

TAAGATTCAA GAAGATTTGG AAAAACGTTT AGAAGAAAAT AAACTCATTC ATAAAGAAAA    3120

ACTAGAACAA ACACTCAAAA AAGAAGTGGA AAAAATGCCT GAGAAATTTA TCGAACAGGT    3180

TGAGATAAAA CGTGTGGAAC AGTTGAAACA ATCAGCTCAA GATGAAATTC GTGACCATTT    3240

ACGAGGGTTT GCAAGAACAA TTCCAAGTTT TATTATGGCT TACGGTGATC AAACTCTAAC    3300

ACTTGATAAT TTTGATGCCT TTGTTCCTGA ACATGTTTTT TATGAAGTAA CAGGGATTAC    3360

GATTGATCAG TTTAGATATT TGCGAGATGG TGGGCAGGAT TTTGCAGGGC ATCTCTTTGA    3420

TAAAGCAACA TTTGACGAAG CTATTCAAGA ATTTCTTCGC AAGAAAAAGG AGTTGGCGGA    3480

TTATTTTAAA GATCAAAAAG AAGACATTTT TGACTATATT CCACCGCAGA AGACCAACCA    3540

AATTTTCACT CCTAAACGAG TGGTGAAAAG GATGGTAGAT GATTGGAAAA AGGAAAATCC    3600

AGGGATTTTT GATGATCCAT CTAAGACTTT TATTGATTTA TATATGAAGT CAGGCCTCTA    3660

TATTGCAGAA CTTGTGAAGC GGTTATATAA TAGCAATGGC TTGAAAGAGG CCTTTCCAAA    3720

TCCTGAAGAA CGCTTAAAAC ATATTTTGGA AAAGCAAGTT TATGGATTTG CTCCGTCTGA    3780

GATTATCTAT AACATTTCCA CTAATTTTAT ATTTGGCAAT CTTTCTAAAG ATATCAGTAG    3840

GAAGAATTTT GTTTTAGCAG ATACCATTCC AGCGGCTAAA GAAGGGAGCA TTCAAAAGTT    3900

GGTTGATTCC TATTTTGAAA ATAATTAAAA AGAAGGCCGA GTCAAAATTC TTTGAAATCA    3960

GAAAAAACGC ATAATATTGA GTGCTTTTGT ACTGCCCCCC AAAAGTTAGA CAGAAAAAAT    4020

CTAACTTTTG GGGGGCAGTT CAGACAATCC TTGGTATTAT GCGTTTTATT GTGGGAAGAT    4080

GTATAATGGA TTGAAATAAG ATATGAACAA ATCAATTAGG AATTTAAAGC ATTTTATAAC    4140

AACGTTTTAG AGTAATGGGG GGCTATTTCA ACTTCAACCT ACTATAATAC AGAAAAAAAC    4200

AACTCCCTGA TAATTCAAGG AGTTGTCTAT AGTTAAATTA GTTTTTAGAA GCTTCTTGGA    4260

ATTCTGGGTT TTTCCATGCT TCGTCAATGA TAGCTTGTAA TTCTTTAGCA GATGCTTGCA    4320

TTTTTTGAGT TTCTGCGTCG TTCAATGGGA TATTTACTGG ACGAACGATA CCATGTGCAC    4380

CAACAACAGC TGGTTGACCG ATAAAGACAT TCTCAACTCC GTATTGACCT TCTTGGAATA    4440

CTGAAAGTGG AAGTACTGCG TTTTCATCGT CAAGGATTGC TTTAGTGATA CGAGCAAGGG    4500

CTACTGCGAT ACCGTAGTAT GTTGCACCTT TTTTGTTGAT GATTGTGTAG GCTGCATCAC    4560

GAACACCTTC GAACAATTCA ATCAATTCAG CTTCTTGAAC ATTTGAGTG TCTTTAAGGA     4620
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1246

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ATTCTTCAAG GTTTACACCA GCGATGTTAG CGTGTGACCA AACAGCGAAC TCAGAGTCAC        4680

CGTGTTCACC CATGATGTAG GCGTGCACTG AACGAGCATC CACATCCAAT TTTTCAGCAA        4740

GTGCTTGACG GAAACGAGCT GAGTCAAGTG AAGTACCTGA ACCGATAACG CGTTCTTTAG        4800

GGAAACCAGA GAATTTCCAA GTTGAGTAAG TCAAAACGTC AACTGGGTTA GCAGCAACAA        4860

GGAAGATACC TTTGAAACCA GATTCAACAA CTTGAGTTAC GATTGATTTG TTGATAGCAA        4920

GGTTTTTACC TACAAGGTCA AGACGAGTTT CACCTGGTTT TTGAGGTGCA CCTGCAGTGA        4980

TCACAACAAG GTCAGCGTCT GCACAGTCAG AGTATTGAGC TGCATAGATT TTTTTAGGTG        5040

AAGTGAAGGC AAGGGCGTGA CTAAGGTCAA GCGCATCACC AACAGCTTTT TCATGCAATT        5100

GTGGAATTTC GATAATTCCA AGCTCTTGTG CAATTCCTTG GTTAACAAGT GCAAAAGCGT        5160

AAGATGAACC TACAGCACCA TCACCGACAA GGATAACTTT TTTGTGTTGT TTAGTTGAAG        5220

TCATTGTTTT AAACATCTCC TTAATTTTAT TAGGGGATTT TCCCTAGACA ACTTCATT        5278
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(2) INFORMATION FOR SEQ ID NO: 228:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1941 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

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ATAAGGAATC TCTAAAAAAT TTTAAGGAGA ATCTAGCAAA TGGATTTCAC ATGGGCACTG          60

AAGTATGCCA CTGAATTTTT GGGAACTGCC ATTTTGATCA TTCTTGGGAA TGGTGCAGTT         120

GCCAACGTTG AACTTAAAGG TACGAAAGGT CACCAAAGTG GCTGGATCGT CATCGCTGTT         180

GGTTATGGTA TGGGGGTTAT GATCCCAGCC TTGATGTTTG GTAACGTATC TGGGAATCAC         240

ATCAACCCTG CTTTCACTCT AGGGCTTGCA GTTAGCGGTC TTTTCCCTTG GGCACAAGTG         300

GTACCTTACA TTATCGCGCA AGTCTTGGGG GCTATCTTTG GCCAAGCCTT AGTTGTGGCA         360

ACATACCGTC CATTCTACTT GAAAACTGAA AACCCAAATA ACATCTTGGG AACTTTCTCA         420

ACTATTTCAA GTATTGACCA TGGTACAAAA GAAAGTCGCT ATGCAGCAAC TGTCAATGGT         480

TTGATTAATG AGTTTGTTGG TTCATTTGTT TTGTTCTTTG CAGCTCTTGG TTTGACTAAA         540

AACTTCTTTG GTGCTGAAGT GCTTCAATTC ATGAAACAAA AGGCAACAGA AGCAGGACAA         600

ACAGTTGATT TTTCTGACTT GGCTATTAAA GCACAGGTGG CTCCACACAC TGCTTCAGGA         660

CTTTCTGTGG CTCACTTGGC ACTTGGATTC CTCGTTATGG CTTTGGTAAC ATCACTTGGA         720

GGACCTACAG GACCTGCCTT GAACCCAGCC CGTGACTTGG GACCACGTCT CCTTCATGCT         780
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1247

TTCCTTCCCA AATCAGTTCT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATTCTTGG   840

GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CAAATTCCTT   900

TATCTCTAAG AAATAGCTCC TTTAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA   960

TCAGACTGGk TCTCTCTTTT kGATTTTTaG GGAAATGAAA GAAcTCTAAA CAAACTCCTC   1020

TCCAGCAGTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT   1080

GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTGGTT TGAATTCTCC   1140

AATCAAATTG TGCAGTTTTC ATTCTACTAT ATATTATCGG AATATTATCG GAGATGGGTT   1200

CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTTGG AATAGTCCTC CCTTCTTTCT   1260

CAAACATTGT GAGGAATTGA TTTACCTTCC TCAACAAAAT GTTCAGTTTC TATTTCATTT   1320

TACTATAAAA TAAGCGATTA GGGGGGGCTAT TCTTCGACCT ACATTGACTC TGCTGAGTCC   1380

TATGATTGTT ATCGTTTTAT CTGCAATTTT ATACTCAATG AAAATCAAAG GGCAAACTAA   1440

GAAGCTAGCC GCAGGTTGTT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAAACTAG   1500

AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT   1560

TGCCCTATTC TTGTTTCATT TTACTATATA AACCAGAGAC TGTTTACATT TTCAGCAAGT   1620

GAGTGGATGG ATAATGCTGA AAACTCCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA   1680

ATTAGTTAAA TTTTTACCAA GAATAATTCA CAAAAACGTT GTAAAACACT TGCAATTTAG   1740

CTGAAATTTG ATAAAATAGT AAGGAAAGTT AGACTGTATT GCCTACTGTC TATCTATAAA   1800

ATATATTTTA TTGGAGGCTT TTACTCAAAT GGCAAAAGAA AAATACGATC GTAGTAAACC   1860

ACACGTTAAC ATTGGTACTA TCGGACACGT TGACCACGGT AAAACTACCC TAACTGCAGC   1920

TATCACAACT GTTTTGGCAC G   1941

(2) INFORMATION FOR SEQ ID NO: 229:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 755 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTTGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTTGG GGGAAGTTTT   60

ACTTGGAACT GGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTTAAAAAG ATAGGGAGTG   120

ATAATCATGC AAGATAACTT TTTATTTGAG GAAATTGAAG AAATTTCAGT ACCAGTTAAT   180

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                                      1248
GATTTTTCAG CTGGACTTGC AACAGGTATC GGATTTGGTT TAGCAATCCT TGCTCTTGCT      240

GGTTGTTGAA GTTTGTTCAT TTACTAACAT CAAGCTTTTT CAATTTCATT TTAGACAGTC      300

ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT      360

TGATTGCGGA CTGAGGGACT AGAGTATGTT TTACTTAACC CCTCTTTTAT TTATTAAAGG      420

TTAGGTTTGT TATGAGAATT GTTGATAAGA TTAAGATATT ACCTACTCCT TATGAGGGAC      480

ACTATCATTT ATATATACCA TCCAGTAAGA AACATGTATT AGTTGGGAAA CAGGAAAAAA      540

ATGGTTAGAG CAACTAATAG GTCAAGAATT TACCATATCG GACTTATTAG TGTTAGTAGG      600

GAAGAAATAT TTTTAAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AAATTAAACT      660

ATAAAAGATT TAATAAGAAT TTTGAAAAAA TCCTATCTTG TTGTCATTAT ATTTGCAACG      720

ATACATGAAA TTAGTCATGC AATAATTGCT AATAA                                 755
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(2) INFORMATION FOR SEQ ID NO: 230:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1483 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```
CCAGAAAAAC CGTAGTGGAG CTCGTGGAAC AGTGGAATTG ATTTTCCAAA AAGAATACAA       60

TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAAGATGTC AGATGCATTT ACAGATGTAG      120

CCAAGATGAA AAAAATCAAA GAAGAAATCA AGGCACATGA GGGACAAGTC GTAGAAATGA      180

CTTTGGAGAA TGGTCGTAAG CGCCAAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC      240

CATCTCTATT TATTGTGGAG TTTGGGGATG TGGAAGGAGA TAAACAAGTT AATGTTTACG      300

TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTCAT TATCTTGACT      360

AAAGTGAGAA ATTTTCTCAC TTTTTCTTTT TTCTCCGAAT AATTTAGGTG AAGGCAATCA      420

TCGCTTTATA TTATTTTTCA AGGAGGAAGA ATGAAAATTT TACCGTTTAT AGCAAGAGGA      480

ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTC CTTTTTTAGT AGTAGGATTG      540

ATGCTAGCAG CTGGTGATAG TGTCTATGCC TATTCCAGAG GAAATGGATC GATTGCGCGT      600

GGGGATGATT ATCCTGCTTA TTATAAAAAT GGGAGCCAGG AGATTGATCA GTGGCGCATG      660

TATTCTCGTC AGTGTACTTC TTTTGTAGCC TTTCGTTTGA GTAATGTCAA TGGTTTTGAA      720

ATTCCGGCAG CTTATGGAAA TGCGAATGAA TGGGGACATC GTGCTCGTCG GGAAGGTTAT      780

CGTGTAGATA ATACACCGAC GATTGGTTCC ATTACTTGGT CTACTGCAGG AACTTATGGT      840
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1249

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CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT        900

GGTTATACAG AATCCTATAA TAAACGAGTT ATAAAAGCAA ACACGATGAC AGGATTTATT        960

CATTTTAAAG ATTTGGATGG TGGCAGTGTT GGGAATAGTC AATCCTCAAC TTCAACAGGC       1020

GGAACTCATT ATTTTAAGAC CAAGTCTGCT ATTAAAACTG AACCTCTAGC TAGCGGAACT       1080

GTGATTGATT ACTATTATCC TGGGGAGAAG GTTCATTATG ATCAGATACT TGAAAAAGAC       1140

GGCTATAAGT GGTTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCAATTGGAG       1200

GCTGTGAATA AAAATCCTCT AGGTAAtTCT GTTCTTTCTT CAACAGGTGG AACTCATTAT       1260

TTTAAGACCA AGTCTGCTAT CAAAACTGAA CCCCTAGTTA GTGCAACTGT GATTGATTAC       1320

TATTATCCTG GAGAGAAGGT TCATTATGAT CAAATTCTCG AAAAAGACGG CTACAAGTGG       1380

TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AGCTAGAGGG AGTGACTTCT       1440

TCACAAAATT ATCAGAATCA ATCAGGAAAC ATCTCTAGCT ATG                         1483
```

(2) INFORMATION FOR SEQ ID NO: 231:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1027 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```
CCCGGAAAAC AAGTTAAAGT TGAAGTTGGT CAAGCAGTTT ACGTTGAAAA ATTGAACGTT         60

GAAGCTGGTC AAGAAGTTAC TTTTAACGAA TTGTTCTTGT TGGTGGTGAA AACACTGTTG        120

TCGGAACTCC ACTTGTTGCT GGAGCTACTG TAGTTGGAAC TGTTGAAAAA CAAGGAAAAC        180

AAAAGAAAGT GGTTACTTAC AAGTACAAAC CTAAAAAAGG TAGCCACCGT AAACAAGGTC        240

ACCGTCAACC ATATACAAAA GTTGTCATCA ACGCAATCAA CGCTTAATTT TAAGGAGAAC        300

ACATGATACA GGCAGTCTTT GAGAGAGCCG AAGATGGCGA GCTGAGGAGT GCGGAAATTA        360

CTGGACACGC CGAGAGTGGC GAATACGGCT TAGATGTCGT GTGTGCATCG GTTTCTACGC        420

TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTTGCAGG CTATGAACCA ATCCTAGAAT        480

TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC        540

AGAGAGAAAT GACCCAGTTA TTCTTTGAAT CATTTTTCTT AGGTATGGCA AACTTATCGG        600

AGAACTATTC TGAGTTCGTC CAAACCAGAG TTATCACAGA AAACTAACAC GGAGGAAAAC        660

ATTATGTTAA AAATGACTCT TAACAACTTG CAACTTTTCG CCCACAAAAA AGGTGGAGGT        720
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1250

TCTACATCAA	ACGGACGTGA	TTCACAAGCA	AAACGTCTTG	GAGCTAAAGC	AGCTGACGGA	780
CAAACTGTAA	CAGGTGGATC	AATCCTTTAC	CGTCAACGTG	GTACACACAT	CTATCCAGGT	840
GTAAACGTTG	GTCGTGGTGG	AGATGATACT	TTGTTCGCTA	AAGTTGAAGG	CGTAGTACGC	900
TTTGAACGTA	AAGGACGCGA	TAAAAAACAA	GTGTCTGTTT	ACCCAATCGC	TAAATAAAAA	960
GGTCCATTGA	ACCTTTTATC	CCGAACCTTG	AAATGTAGAG	GTGAGGAAGC	TAGAAACAGC	1020
TTAAAAT						1027

(2) INFORMATION FOR SEQ ID NO: 232:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1990 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAAAT	GGTGCAGGTA	AATCTACGTT	AATTAATTCT	ATTGTAGGTT	TTCAAGAGAT	60
TTATTTAGGA	GAAATAGAGT	ATTGTGATAA	AGATTTGATA	GTTAGTTCTC	AACCTTTTGC	120
TCATTTAGGC	TTTACTCCTC	AAACCACAGT	AATTGATTTT	TATACTACTG	TGAAGGACAA	180
TGTAATATTG	GGGCTGAACC	TTGCTGGAAA	GTTTGGGAAA	AATGCTGAGA	AGTTGTGTCA	240
AATAGCCTTA	GAAATTGTTG	GGTTAGCTGA	TAAAAAAAAT	AATTTGGTAG	AAACATTGTC	300
AGGTGGACAA	CTGCAACGCG	TCCAGATTGC	TAGAGCAATA	GCTCATAATC	CAGATTTTTA	360
TATTTTAGAT	GAACCTACCG	TTGGTTTAGA	TACTGAATCT	GCCGAAAAAT	TTTTAATGTA	420
TTTAAAAGAT	AAGAGTTTGG	AAGGAAAAAC	TATTATCATA	TCTTCACATG	ACATAAATCT	480
ACTCGAAAAG	TTTTGTAAAA	AAATACTTTT	TTTACAAAAT	GGCTCCATAT	CATTTTTTGG	540
TGATATGCGT	GACTTTGTAG	ATAATTCAAC	TATCAAATTA	AATTTTTCAA	TGCAGAATAG	600
AATTTCTAGA	TATCAAATTG	AATTTTTAGA	AAATTTTAGA	TTTAAAGTTC	ACATCGAAGA	660
TAATGATAGT	TTTACAATAG	AAGTCCCTAT	AGAAGAAAAG	ATCTTAGATG	TTATCAATGA	720
GGTAGGAAAA	GCATGTGAAA	TTAAAAACTT	TTCAACAAGT	AAATTAACCT	TACAAGAAAG	780
TTATTTGCAA	AGAATAGGAG	GAGAAAAATG	AAGGCTGATC	AATTAAGGCA	CAAATCGGAC	840
TTAGGTTTAA	GAGGTCTAGC	GATTATTGCT	AAAAATGAGA	TTATTGCTTT	TTTTAGAAGT	900
AAAGGTTTAA	TTATTTCTCA	GTTTCTACAA	CCAATCTTAT	ATGTTGTTTT	TATAATAATA	960
GGATTAAATT	CTTCGATAAA	GAACATTCAG	TTTAATGATA	TAAAAACCTC	TTATGCAGAA	1020
TATACAATCA	TTGGTGTTAT	AGCTTTATTG	ATAATCGGGC	AGATGACTCA	AGTTATTTAT	1080

1251

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AGGGTGACAA TAGATAAAAA ATATGGGCTA CTTGCTCTTA AGTTATGCAG TGGAGTTCGT     1140

CCTTTATATT ATATTTTAGG GATGAGTATC TATTCTATAT TAGGGTTGAT AGTTCAAGAA     1200

ATTATTATAT ATATAATTAC GTTAGCGTTT GAGATAAAATA TCGCAATGGA TAGATTTTTT    1260

TATACAGTTT TGTTATCTAT TGTTGTTTTA TTATTTTGGG ACTCCCTTGC AATTTTACTT     1320

ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTTGT ACTAACACCG     1380

CTTGGTTTTA CAGCTCCTGT TTTCTACTTA ATAGATTCTG CTCCTAGTAT TGTGAGATGG     1440

ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAACTATTT TGAGAAACTT TTATTTTAAA     1500

AATTCAACAA CTTTGGAATT AGTTTTCTTA TTGTTAACAT CATTACTTGT CCTTATATCT     1560

GTATCTTTTA TTATACCAAA GATAAAATTG ATACTGATAG AAAGATAAAA GTTGGGTCAT     1620

CCAACTTTTT TGTTGTCTCC CGAAAACCAC TAGCTATGCT AGTGGTTCCA TAGAGCTTTT     1680

AGCGTGGTAA CAAAAAGAAC CTCCTAAAAT GATAAGATAG AAGTGGTTTC TCCGCCACTA     1740

CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAA CAAAGTTTAT CACATACCAC     1800

ATGGAATTGT AAATATCATA TTGTTTTTGC ACCCAAATAT CGTCGTCAAA TCATTTATGG     1860

CAGATACAAA GCTAGTATCG GAAGAATCAT ACGTGACTTA TGTGAGCGTA AGGGTGTAAT     1920

AATCCATGAA GCGAATGCTT GTTCAGACCA TATTCACATG CTTATCAGTA TTCCTCCGAA     1980

ACTTAGTGTT                                                           1990
```

(2) INFORMATION FOR SEQ ID NO: 233:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 4766 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

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GAACTATATT GCATATATTT CTAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT       60

ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCGCCCATAT TTAGGTCCTG GACGTGGAAT      120

CATTGAAAGC TCAACTGGAC GTATTCTTAT TCCGTCTTAC ACTGGTAAAG AGTCTGCGTT      180

CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTTCTAG      240

TTGGTCAGCA GAAGCACAAT TTGTAGAATT GAGTCCAGGA GTAATTCAAG CATATATGCG      300

TACAAATAAT GGTAAAATTG CATATTTAAC AAGTAAAGAC GCAGGTACTA CTTGGAGTGC      360

ACCGGAATAT TTGAAATTTG TTTCAAATCC AAGTTATGGA ACACAATTAT CAATCATCAA      420
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1252

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TTATAGCCAA TTGATTGATG GTAAAAAGGC TGTCATTTTA AGTACTCCAA ACTCCACAAA   480

TGGTCGTAAA CACGGACAAA TTTGGATTGG TCTAATTAAT GATGATAATA CAATTGATTG   540

GCGTTATCAT CACGACGTTG ATTATAGTAA CTATGGATAC TCATATTCAA CATTGACAGA   600

GTTACCAAAT CATGAAATTG GATTGATGTT TGAAAAATTT GATTCATGGT CTCGTAATGA   660

ACTTCATATG AAAAATGTTG TACCATATAT AACATTTAAG ATTGAAGATC TGAAAAAGAA   720

TTAAAGCTGA AATTTGAAAA TATATAAAAA GAGGATAAAA ATTATGGTAA ATTACGGTAT   780

TGTTGGAGCT GGATATTTTG GAGCTGATTT AGCTCGCTCA ATGAACAAAA TTGAAGATGC   840

AAAAGTGGTT GCGGTATTTG ACCCAAATCA TGGAGAAGAA GTTGCTCAAG AGTTGGGATC   900

AGATGTTTGT GCAAGTTTAG ATGAACTTGT AGCACGTGAA GATATTGATT GTGTGATCGT   960

AGCTTCACCT AGCTACCTTC ACCGTGAACC AGTTGTGAAA GCTGCTCAAC ATGGCAAACA   1020

CGTATTTTGT GAAAAGCCAA TTGCATTGTC TTATGAAGAT TGTAAAGCCA TGGTTGACGC   1080

ATGTAAAGAA AATAATGTCA TCTTTATGGC TGGTCACATC ATGAACTTCT TTAACGGTGT   1140

ACACCATGCT AAAGAATTGA TTACTCAAGG TAAAATCGGT AAAGTTCTTT ATTGCCATGC   1200

TGCTCGTACA GGTTGGGAAG AACAACAACC AACTGTATCA TGGAAGAAAC TTCGTTCTCA   1260

ATCTGGAGGA CATTTGTACC ACCATATTCA TGAATTAGAT TGCATTCAGT TTATCATGGG   1320

AGGACTTCCT GAAAAAGCGA CAATGGTAGG AGGCAATGTA TATCATAAAG GTGAAAACTT   1380

TGGTGATGAA GATGATATGC TCATTGTAAA CTTAGAATAC TCTGATGATC GTTATGCTGT   1440

TTTGGAATAT GGTAATGCTT TCCGTTGGGG TGAACACTAC GTCTTGATTC AAGGAACTGA   1500

AGGAGCTATC AAACTTGACT TGTTCAATAC TGGCGGTACT CTTCGTGTTA AAGGTGAAGG   1560

AGAATCACAC TTCTTAGTTC ATGAAACTCA AGAGGAAGAT GATGATCGTA CAGCTATCTA   1620

TACCGGTCGT GGTATGGATG GAGCAATTGC GTACGGTAAA CCAGGAGTAC GTTGCCCATT   1680

ATGGTTGCAA ACATGTATTG ATAAAGAAAT GGAATATCTA CATGACATCA TTAAAGGTGG   1740

AGAAATTACA GAAGAATTTG AAAAACTTCT CAATGGTGTA GCTGCTTTAG AATCAATCCC   1800

TACCGCTGAT GCATGTACTT TATCAGTTAA AGAAGATCGA AAAGTAAGTC TTTCAGAAAT   1860

CACAAATGCT TAACTTTTGT AAAACAGAAT AGTAAATTCT TGTCATTATA TAATTTCTAA   1920

AGTTCTGTGA TACAACTCAT TGAATAAAGA AATAGAGATG GGACTGGGAT AATGCCCAGT   1980

CCCATTTTTT ATCAAAAAGT AATGAGATCA AAAATGTGGG AGTGTTGAAA TGAAGATTAT   2040

AGGTATCGAT ATTGGCGGAA CAACAATTAA GGCAGATTTA TACGATGAGT TTGGAACGAG   2100

TTTGAATCAT TTCAAAGAGA TAGAAACAAT TATTGACTAT GATTTGGGAA CGAATCAGAT   2160

ATTAAATCAG GTCTGTGATT TAATTGGTGA GTATACTTTA AATCATTCAA TTGATGGTGT   2220
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1253

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TGGGATTTCC ACTGCTGGAG TTGTTAATGC TAATACTGGA GAAATCATCT ATGCAGGCTA    2280

TACAATACCA GGGTATATCG GAGTAAACTT TACTGCCGAA ATAGAAAAAC GTTTTGGGTT    2340

GTATACTTTT GTTGAAAATG ATGTTAATTG TGCTGCATTA GGTGAATTGT GGAAGGGACA    2400

AGCCAAAGAT AAGAAAAATG TAGTAATGGT TACTATTGGA ACAGGTATAG GAGGCAGTAT    2460

TATTGTCAAC GGACAAATTG TTAACGGATT TAACTATACT GCTGGTGAAG TAGGTTATAT    2520

TCCTGTAGGT AATTCGGATT GGCAAAGTAA AGCCTCAACA ACCGCATTGA TTCATTTATA    2580

TCAAAAAAAG AGCTTGAAAA CTAATCAAAC TGGACGTACT TTCTTCACTG ATTTAAGATC    2640

TGGAGATAAA GTTGCTGAAG AAACTTTTGA AATTTTTGTA GAAAATCTAA CAAAAGGTTT    2700

ATTAACGATT TCTTATCTAC TTAATCCAGA AATTCTCATA TTAGGAGGTG GGATTCTGGA    2760

TAGTAAGGAT ATTTTGTTAC CTGAAATTCA AAGTTCTTTA GCTAAAAATG CAATGGATAA    2820

TAGGTTTTTA CCTAAAAATC TTGTGGCAGC TACATTAGGA AATGAAGCTG GTCGTATAGG    2880

AGCTGTAAAA AATTTCTTAG ATAGAATTTC TAATAAATAG TATGTAAGAT AAGGAGGTGT    2940

CACAATGACT AACTCTGTAT TTTCGACAAT GCAAGATATT GAGAATGTTG CAACCGATAT    3000

TATAAAATCA TATGATAATG AGATTTATAC TTATAAAGCT GTTTCCCAAG AAGAATTGGA    3060

AAAACTAGAA AAAAGTTATG ATGAAAAAAG TCACGAAGAA TTAGTTTCAA TAGAAAGCAA    3120

TTTAGAAATG AAACAACAGA ACCTTATTGA TGAGGTTAAT AAAACAATCA AGGAAAATGA    3180

TGCAAATATT CAGTATATTT CATCAAGTAG GAGAGGAGAA TTTGTAGAAA AAATTATTGG    3240

TAGGGTGGTA GAAAAATATG GCCATTAGTC AGATGAAAAG AATCTCTCTA CTATTTTCTA    3300

AAAGTAGTCT TGATGATGTT TTAAAAACTA TTCAAGAACT AGAGTCAGTG CAGTTCCGTG    3360

ATTTAAAGGT TCAGGATAAC TGGTCAGAAG CTCTAGAAAA AGATGAAGTT GTATTTCCAA    3420

CTATTCAAAT TTTTCATACT TCTAATTCCA ATCATGGGGT TATTGAGGGA AATGATGCCT    3480

TGACTTATTT GATGAATCAA CAACAACATT TAGAAGCAAC TGTAGAGAAA TTACAAGAAT    3540

ACCTACCGAA AGAAAACACG TTTAAATTAT TGCAGCAACC TCCGATAACT ACCTCTTATG    3600

AAGAATTAGA GAAATTTGGT AAAGCTAATG TTGCTGAGGG TGTTCTTAAA AAAGTGAATC    3660

ATCAAATTAA CAGAGTTCAT GAATTAGAAA GACACATTCA AGTAATAAT GAGGAAATAG    3720

AGCGATTAAT AAAGTGGGAA AAATTAGAAA TTGTTCCTGC GAATTTAGAA CAATTTTCTT    3780

TCTGTAAAGG AAAAGTCGGA ACAATTCCAA GGACTGAAGA TAATCGCTTA TACAATAGTC    3840

TTTTAGAAAA CAATATTGAA GTTCAAGAAA TATTTTCTAA TGATAGAGAG TACGGTGTTG    3900

TTGTTTTCTA TCAGTCTAGT TACTCTATAG ATTTTGATGA ATACTTATTT GAACCATTTG    3960
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1254

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ATTATTCTAG AAAGGAATTA CCGAAGCAGC GAGTAGTAGA TTTAGATCAA GAAAACATGC    4020

AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATATTTGA    4080

TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTCGTCAA ATCTCTAAGA    4140

ATAACTTTTT GTGCACTCCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA    4200

TTTTATATTT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTTAT ATTTATGAAT    4260

CGGAAACATT GACGGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCTTTAA    4320

TTGAACCATT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTAT GAGAAAGATC    4380

CTACACCTGT ATTAGCACCA TTTTACTTTA CATTTTTTGG AATGATGGTT GCTGATTTAG    4440

GCTATGGTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTTT CATCTACCTT    4500

CAGCAACTAA GAGATTTTTA AAATTCTTTA ATATATTAGG GGTAGCCGTT GCAATTTGGG    4560

GTGGAATCTA TGGCTCATTT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACCT    4620

CTGATGTCAT GACTATATTA GTAGTGTCAG TTGTGTTTGG GTTTATTACA GTATTTGCAG    4680

GTTTGTTAGC TTCAGGACTA CAAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT    4740

CAGGATTTGC GTGGTGTGTT ATTCTG                                        4766
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(2) INFORMATION FOR SEQ ID NO: 234:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2484 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```
CCTTTTAGAA AAAATTAAAG AATACGACAC CATTATCATT CATCGTCATA TGAAACCAGA     60

CCCTGATGCC TTGGGAAGTC AGGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCCAGA    120

AAAAACCATC AAAGCCGTCG GTTTTGATGA ACCAACTCTT ACTTGGATGG CTGAGATGGA    180

TCTTGTTGAA GATAGAGCCT ACCAAGGCGC ACTTGTCATC GTCTGTGATA CAGCTAATAC    240

TGCTCGTATC GATGATAAGC GCTATAGTCA AGGTGATTTT CTCATTAAGA TTGACCACCA    300

TCCAAATGAT GATGTATACG GTGACCTGTC TTGGGTCGAT ACTAGTTCAA GTAGCGCTAg    360

aGaTGATTAC CCTATTTGCC CAAACAACCC AACTAGCCTT GGCAGATCGC GATGCTGAGT    420

TGCTCTTTGC AGGAATTGTC GGTGATACAG GTCGCTTCCT CTACCCTTCT ACCACTGCAC    480

GGACTCTTCG CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC    540

GCAAAATGGA CACTATGAGC TACAAAATTG CTAAACTGCA AGGCTACATC TACGACCATC    600
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1255

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TGGAAGTGGA TGAAAATGGT GCTGCTCGCG TTATCCTGAG TCAGAAAATC TTGAAACAAT    660

ACAATATAAC CGATGCTGAA ACTGCGGCCA TTGTAGGTGC ACCTGGACGC ATTGACAGAG    720

TGAGTCTCTG GGGAATTTTT GTCGAACAGG CTGATGGCCA CTACCGAGTT CGCTTACGCA    780

GTAAAGTCCA TCCTATCAAT GAAATTGCCA AGGAGCATGA TGGTGGAGGC CACCCTCTAG    840

CAAGTGGTGC TAATTCCTAT AGCCTAGAAG AAAACGAAAT CATCTACCAA AAGTTAGAAG    900

ACTTGCTTAA AAACTGATAA AATACTTGCC AAACTTTTCA GAATCTGATA GACTAGTATA    960

GTAACAATCT ATGGCTCGCA AAGAGACCAT GGCAGAAAGG AAATATTGCA AAATGAAAAr   1020

AGATATCCAT CCAGAATATC GCCCAGTTGT CTTCATGGAC ACAACTACTG GTTACCArTT   1080

CCTTAGCGGT TCAACAAAAC GCTCTAACGA AACAGTTGAG TTCGAAGGCG AAACTTACCC   1140

ATTGATCCGT GTGGAAATTT CATCAGACTC ACACCCATTC TACACTGGAC GTCAAAAGTT   1200

CACTCAAGCA GATGGACGCG TGGATCGTTT CAACAAAAAA TACGGTCTCA AATAATGATA   1260

AGAGAACAGT TTTGGCTGTT CTTTTTTGTT TCTTGAAATC AACTGCTGTT TTCATGTTCC   1320

AGACTCATCT GTAGGTTCGA TTTCCATGCT ACTAGGCAGG AAGGAAATAG CTGTTTCAAC   1380

ACGTCCATAA TGAGCTATAC TATTGTCACG AACCACACTT TCATTGATGG TCCAAGTGGA   1440

ATTCATTTTC TTAAAAGCTT CTCGGACTTT TTCCAAATCT TTGGAGGCAA TGGCCTGCTC   1500

TAAGGTTTCA AAACGAGGAC TTATACTCAT CTGCTTTCAA AAAGCATTCT AGTCCATCTC   1560

CGATTACCGA TGGACTTTAT CACCTCCTTC TCCAGTCCTT GTATGACATC TTGAAGTTGA   1620

TTCATGACAT CTTCCAAAGT TCgAAAGGCT TTATTCTTAA ATCCACGTTT ACGAATCTCT   1680

TTCCACACTT GTTCAATGGG TTCATCTCTG GTGTGTATGG AGGAATAAAG GTAAAATCAA   1740

TATTAGTCGG AATATTTAAG GTACTTGATT TATGCCATAT AGCATTGTCC ATAACGAGTA   1800

AAAGGATAAG CTTGTGAAAG CTCTTCTAAA AAGGCGTTCA TCCCACACTCC TTTTTATAAA   1860

CCTGAAATAA GGCATCAATT GTAACAAATT CTCCTGCCTC TGTAGCCTTC AAATGACGGG   1920

CAAGAAAGGC TTTCTCTTCC TCAACTGTCA TATATGCATG GTTACGACCA CCACGTGTTT   1980

CTTGAAGGAG AGAGTCGAGT CCGAACTCCT CATATTTTTT TACGTTCGC CAAATCGTTG    2040

TTTGATTACA GTCTAAAAGC TCTATAATCT CTTTATAAGA TTTGCCCATC AGACGAAATA   2100

TAGTAGATTG AAACTAGAAT AGTACACCTC TACTTCTAAA ACATTGTTAG AAATCGATTT   2160

GTCCTGTTCT TGTTTCATTT TACTATAGAA CGATTTGAAG GCGTTTATAA TATTTAGCTG   2220

TACGAGAGTC TTTTAAAAGT GTTTTGATGG TTTGGATTTC TTCTTTAGTT GATTTCATAT   2280

TACTATTATA TAATGCTTTT TGATTTTAGT CTGGTATAAA TATTGCTTTC CTCCAAAATG   2340
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1256

GTCATAGTTT TACTGGCAAA TCTAACATAT CACGGATAAA TTAACAAGTG ATTTCTGAAT   2400

TGCTAAACAT TTTCTTTTCT TATAGCATAC TTTAAGATTT TGTCTTTGAG AAAGATATTT   2460

CCAAGAAAAA CGTTCGTTTT TTGG   2484

(2) INFORMATION FOR SEQ ID NO: 235:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1766 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAGAA   60

AAAATCGAAA AATTAGCTAA GAAATATTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA   120

GTTCGTGAAA TGGCAAATGA TAATAAGAGC CATTATTTGA TATACAGAGT TTTAGGTATT   180

TCATTTGAAG AAGGAGAAAA TATCGATTTG TATCAAAATA AAGGTCGTTT TTTATACAAA   240

TATGCTGGTT CATTTTTAGA AGAAGCTGCA GTACTATGCT TTAACGAAAA ATTTGGTACA   300

GAAAATACTT AAAAAGTTAA CATTCCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA   360

ATTGATTGTT TAGTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA   420

GATGGAGACC ATATAACTAA AGAACACACT AGAATAAAAG TTATTCATAA CAAAGGATAT   480

ATACCAATTC GGTTAATGTT CTACTATCCA AATAGAACTC AAGCTATAAA AATTCAGCAA   540

ACTTTAGAAA CATTGTATAA CGGTATTGGA GGGAAATATT ATTATGGAGA TTCTGCCTGG   600

GAACATTTAA GAGCAGTGAC CGGTATTGAT TTACTTAGTA TTCTAACAGA TATTGCAAAT   660

AAAAAAACAG GGGTAAAATC AAAATGACAG TATTAAAAGG AGATAACTTA GAAATATTAA   720

AAACTATTGA ATCCTCAAGT ATTGATTTAA TCTATATGGA CCCTCCTTTC TTTACACAGA   780

AAACCCAAAA ATTATCTAAT AACAAAAATA TTATGTATTC ATTCGAAGAT ACGTGGACTT   840

CGATTGAGGA TTACAAAGAA TTTTTGTCTG TAAGATTAGA AGAATGCAAA AGAGTGCTAA   900

AAAATAGTGG CAGTATTTTC GTTCATTGTG ATAAAATTGC AAATCATCAT ATTAGATTAA   960

TTTTAGATAA TATCTTTGGA GTAGATATGT TTCAAAGCGA AATTATATGG AACTATAAAC   1020

GGTGGTCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AAACATTTAC TTTTATTCAA   1080

AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGTA TTCTTCTACT ACAAATATCG   1140

ACCAAATACT AGTGGAACGA AAACGAGATG GAAACTCTAA AACTATATAT AAGGTTGATA   1200

ATAATGGTAA CTATATTCTA GCAAAAGAGA AAAATGGAGT TCCCCTTTCA GATGTTTGGA   1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA   1320

TTCTGTTATT AGAACAAATT ATAAAGATTG CTACTGATAA AAATGATATA GTTTTAGACC   1380

CGTTCTGTGG AAGTGGAACT ACTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG   1440

GGATTGATTT ATCTGAGGAA GCTATCAATA TAACTCAGCA ACGTCTGGAA AATGTTATAA   1500

AAACAAGTTC AAATTTATTG AATAAAGGAA TCGAAGCATA TAGAACCAAA ACTGAGGAAG   1560

AGGAAAACAT TCTTAAATTA TTACAGGCAA AAATTGTTCA AAGAAATAAA GGAATTGATG   1620

GTTTTTTACC TAAACATTTT CAAAAAAAAC CGATACCTAT AAAAATTCAA AAAAATAATG   1680

AATGTCTGAA TGAGAGTATC TCTTTATTAC AGAATGCTAT AAACTCCAAA AAACTTGATT   1740

TTGGAGTAGT TATAAAAACT CATTCG   1766

(2) INFORMATION FOR SEQ ID NO: 236:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 748 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAAATCA AATTCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTGCGG   60

CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA   120

GCGCGGAGAA TTTCTAATTC TTCCTTGGTC AAGCGACGCC ATTCCCCTCG TTCTAGGTTC   180

TCATCTAATA CTAAAGTTCC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG   240

TAGCCCACCA TACGCTTGAT CTGATGAAAC TTCCCTTCTG CAATGGTCAC ACGGATTTGG   300

CTTTGATTCT TTTCTGTATC TATGGATACA AGCTCCAGTA TAGCGGGTTG ACAGGTAAAG   360

TCTTTGAGAG GAATACCCTC AGCAAATGTC TCCACATCTT CTTGGGTCAT GATTCCCTTG   420

ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC   480

TGACCATCAT TGGTCAAGAG CAAAAGACCA TGCGTGTCAA TATCCAAGCG TCCTACTGGG   540

AAAACTTCCT TACTCCGCGC CAAGTCATCC AACAAGTCCA GAACGGTTCT GTGCTTGGGA   600

TCCTCAGTCG CTGAGATAAC TCCTTTGGGC TTGTTCATCA TGTAGTAGAC AAACTCTTCA   660

TACTCCAACA CTTGCCCATC AAAGCGAATC TCATCTATTT TTTCATCAAT CTGCAATTTA   720

GCTGATTTTT CTTTTTGACC ATTTACAG   748

(2) INFORMATION FOR SEQ ID NO: 237:

1258
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1449 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```
AAAAGATTAC ATTGCAACAA TTGAAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT      60

TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TCGTTCAGTA     120

TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCGTGGAT TTATCGTGGG     180

TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGCGCCT GTTCGTAAGC CAGGTAAATT     240

GCCACGCGAA GTTATTTCTG CTGACTATGA AAAAGAGTAC GGTGTCGATA CCTTGACTAT     300

GCACGCGGAT GCCATTAAGC CAGGTCAACG TGTTCTTATT GTAGATGACC TTTTGGCGAC     360

AGGTGGAACT GTTAAGGCAA CTATCGAGAT GATTGAAAAA CTTGGTGGTG TTATGGCAGG     420

TTGTGCCTTC CTTGTTGAAT TGGATGAATT GAACGGCCGT GAAAAAATTG GTGACTACGA     480

CTACAAAGTT CTTATGCATT ATTAATGAAA ACAGTCCCTA GGGCTGTTTT CTCTACACTA     540

GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAAACTAT AATTGAAAAC TATATCTTCT     600

TGCAGTATAA TAAAAGGACT AAGTGTTTGA GATTTGTCTT CAAACATATG CAATTATTCC     660

TGAAAGAGTA CAGTTAGGAG AGGGTTATGC CGATTCGAAT TGATAAAAAA TTGCCAGCTG     720

TTGAGATTTT ACGGACAGAG AAATATCTTTG TCATGGATGA TCAACGTGCT GCCCACCAAG     780

ATATCCGTCC TTTGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAATG GTCACAGAGA     840

CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACAACT GGATATTGAT TTTCTCTATA     900

TGGAGAGCCA CCGTTCTAAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAAACTT     960

TTCCTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGGTGCT CCAGTTGAGC    1020

ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGGTCTA    1080

AGACTCATGT CTATTCGACC CTTCATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC    1140

GCTATGGTGT AGAAAAATAC CAGATGGACA GTAAGCTATC AGGTATTTAT CCTCAGGACA    1200

CCCTAAAAGA GGGTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCCTCATT    1260

CACGGCACAC GGAGATTTCT AAGGAAGAGG TCTTAAACAA GACCAATCTC GAGATTTTAT    1320

CAGAAGGACC TCAGGTTGGG GTTTCTATTw TGGCCAGTCG TGATTTACGA GAAATTTATA    1380

GTTTTGGTCA TTTGGAGTAT GACCGTGATA CTTTGGCAAA AGAGTATTTT CGAGATCGTG    1440

ATGCAGGTT                                                            1449
```

1259

(2) INFORMATION FOR SEQ ID NO: 238:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 904 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```
TACCCGCTTC TTTCAAGAGT TGGAGCAGGG CTTGTTTGCG ATCTTTTGTC ATAGTTCTTC       60

CTTTTAACGG CGTTTTCGAA GCACTTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT      120

ACTATGGATA ATTGTACCAA ATCCAACTAG TACAAATAGA ACATAAAACA TATTTTCTAC      180

ATTGGTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGGCATGAAC      240

AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTTGGT TTATCTAGGG TATCGGGGAA      300

TTTTTGTAGG TAAAGAGCTC CTAAAGCACC AAAAGATATA TGGGAAAAAG CCCGAAAAAC      360

GATAACCATG GGATAGCCAG CCATCAAAAA TCCAAAACTA GAGGCTAGGA TGACAAAAAC      420

TGCCATCAAG GGCGACAAGA ACATGGCTAT AAAAATAGCG ATGTGGCTCC CCAAAGTATA      480

GGAAGCAGGT GGAATGACAA TCTTGAAAGG CATAACAATT GGAATCAAAA TCGCAATAGC      540

CGTTAAAAGG GCTGTCATTG TCATAAATTG TGTCTTTTTC CGTGTATTCA CAAGAATCTC      600

CTTTTTAACT GCATATACAC TAGTATGGTA CAATAAACCA GACAATAAAG CAAGAATTTA      660

CTTGGGTTTA TAGATCATTT TTTAGTTAAA AGTTATAGTA GATTGAAACT AGAATAGTCC      720

ACCTCTACTT CTAAAACATT GTTAGAAATC GATTTGGCTG TCCTGATCGA TTTGTCCTGT      780

TCTTATTTCG TTTTACTATA GTAAAGATTT CATTAAAAAG AAACTGTATA GAGCAAAATC      840

TCCACCTTCA GGTTTGGAAA GCGGAGATTG TTTnTTATTT TTTCCAGGGT TTGTAGTCGT      900

GGGA                                                                   904
```

(2) INFORMATION FOR SEQ ID NO: 239:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 946 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
CACTCAAACA TGACTTATAT CAAGACGGAT GGACTTCAAG ACGATGCCAA TCGCTTGAAT       60
```

1260

```
CGTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC        120

CTTCATGGTG GACtTCGTGT ATACGGTGGA ACTTTCTTCG TCTTCTCTGA CTATGTGAAG        180

GCAGCTGTCC GCTTGTCAGC CTTACAAGGA CTTCCTGTGA CTTATGTCTT TACCCATGAT        240

TCAATCGCAG TTGGGGAAGA TGGTCCGACT CATGAACCAG TTGAGCATTT AGCAGGTCTT        300

CGTGCTATGC CAAATCTAAA TGTTTTCCGT CCAGCAGATG CGCGTGAAAC GCAAGCAGCT        360

TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCCC TTGTCTTGAC ACGTCAAAAT        420

TTGACTGTTG AAGATGGAAC AGACTTCGAC AAGGTTGCTA AAGGTGCTTA TGTTGTATAT        480

GAAAATGCAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT        540

GTCTCAGCTG CTAAAGAATT GGCTAGTCAA GGCGAAAAAA TCCGCGTAGT CAGCATGCCA        600

TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAGG AAGAAATTCT TCCAAATGCA        660

GTCCGCCGTC GTGTTGCAGT CGAAATGGGT GCAAGTCAAA ACTGGTACAA ATATGTTGGT        720

CTCGATGGTG CCGTTCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT        780

TGGCAGAATA TGGCTTTACT GTAGAAAATC TTGTAAAGT TGTTCGAAAC TTGAAATAAT         840

CCTAAAAATC AGGGCGTAAG CTCTGGTTTT TCTTACCAGA AAAGTAAGGT ACAATCTTGT        900

AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAAAG ACAAAG                       946
```

(2) INFORMATION FOR SEQ ID NO: 240:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2764 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```
CGGGGCTCCc TAGTTCTTAG GGAGCTATTT TTGTTTTTTC AAGAAGTTAT CTTCTTGTAT        60

TTTATACTCA ATGAAAATCA AAGAGCAAGC TAGGAAACTA GCCGTAssTG CTCAAAACAC        120

TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC        180

GTTGACGCGG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC        240

CAGATTATTC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTAGTTA ACAAGACCTT        300

GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTTGTAACT GGTGGTGTGG        360

TATCGTCCAT TGGGAAAGGG ATTGTGGCAG CGAGTCTAGG CCGTCTCTTG AAAAATCGTG        420

GTCTCAAAGT AACCATTCAA AAGTTTGACC CTTATATCAA TATTGATCCG GGAACCATGA        480

GTCCTTACCA GCACGGGGAA GTTTTTGTGA CAGATGACGG AGCTGAGACA GATTTGGACT        540
```

1261

```
TGGGTCACTA TGAACGTTTC ATCGATATCA ATCTCAACAA ATATTCCAAC GTGACAACTG        600

GGAAAATTTA CAGTGAAGTT CTTCGTAAAG AACGCCGTGG AGAATACCTT GGGGCAACTG        660

TTCAAGTCAT TCCTCATATC ACAGATGCTT TGAAAGAAAA AATCAAGCGT GCCGCTCTAA        720

CGACCGACTC TGATGTCATT ATCACAGAGG TTGGTGGAAC AGTAGGAGAT ATCGAGTCCT        780

TGCCATTCCT AGAGGCTCTT CGTCAGATGA AGGCAGATGT GGGTGCGGAT AATGTCATGT        840

ATATCCATAC AACCTTGCTT CCTTACCTCA AGGCTGCTGG TGAAATGAAA ACCAAACCAA        900

CCCAACACTC TGTCAAAGAA TTGCGTGGCT TGGGAATCCA ACCAAATATG TTGGTTATTC        960

GTACAGAAGA GCCAGCTGGT CAAGGAATTA AAAATAAACT GGCCCAGTTC TGTGATGTGG       1020

CACCAGAAGC CGTTATCGAA TCGTTGGATG TTGAACACCT TTACCAAATT CCACTGAACT       1080

TGCAGGCACA AGGGATGGAC CAAATTGTTT GTGATCATTT GAAATTAGAC GCACCAGCAG       1140

CGGATATGAC AGAATGGTCA GCCATGGTGG ACAAGGTCAT GAACCTCAAG AAACAAGTTA       1200

AGATTTCCCT TGTTGGTAAG TATGTGGAGT TGCAAGATGC CTATATCTCA GTGGTCGAAG       1260

CCTTGAAACA CTCTGGCTAT GTCAATGATG CAGAAGTTAA AATCAATTGG GTCAATGCCA       1320

ATGATGTGAC AGCAGAGAAT GTAGCAGAAC TCTTGTCTGA TGCGGACGGG ATCATCGTAC       1380

CAGGTGGTTT TGGTCAACGT GGTACAGAAG GGAAAATCCA AGCCATCCGC TATGCGCGTG       1440

AAAATGATGT TCCAATGTTG GGAGTCTGCT TGGGAATGCA GTTGACATGT ATCGAGTTTG       1500

CTCGTCACGT TTTAGGTCTT GAAGGTGCCA ATTCTGCAGA GCTTGCACCA GAAACAAAAT       1560

ACCCTATCAT TGATATCATG CGTGATCAGA TTGATATTGA GGATATGGGT GGAACCcTTC       1620

GTTTGGGACT TTATCCGTCT AAGTTGAAAC GTGGCTCTAA GGCTGCTGCT GCTTATCACA       1680

ATCAAGAAGT GGTGCAACGC CGTCACCGTC ACCGTTATGA GTTTAATAAT GCCTTCCGTG       1740

AGCAGTTTGA GGCAGCAGGT TTTGTCTTTT CAGGAGTTTC TCCAGACAAT CGTTTGGTAG       1800

AAATCGTGGA AATTCCTGAA AATAAATTCT TTGTAGCTTG TCAGTATCAC CCTGAACTGT       1860

CAAGCCGTCC AAACCGACCA GAAGAACTCC ACACTGCCTT TGTTACTGCA GCAGTTGAGA       1920

ACAGCAATTA GCAAAATCAG AACCTTTGAG AAAAATCTCA GAGGTTTTTT GCATACGATG       1980

ATATTGCAGT ATATCTGAGG TAGGGGTCCT CTGTATGTAC CTGCTACCGT TGAAATCAAT       2040

AGCGACTCCC TCTTGCCCTG TGCTAGTGAA TGGATTTATC AGTATATTGA AATGAAATAA       2100

AATTTGAACA AATTAATTCG GAAAGCCAAA TCAATTTCTA GCAAAGTTTT AGGAACTGGA       2160

TTGTATAGTG AATTGAAATA AGATGTGAAC ATCTCTATCA GGAAAGTCAA ATTAATTTAT       2220

AGAAATATTT TAGCAGTCAA GATGTACTGT TATAGATTCA ATACATTATA CTTTTTTAAT       2280
```

1262

```
TTAATCCACT ATAGTAAAAT GAAATAATAA CAGGACAAAT CGATCAGGAC AGTCAAATCG     2340

ATTTCTAACA ATGTTTTAGA AATAGAGGTG TACTATTCTA GTTTCAATAT ACTATCCCAA     2400

ATCATTCATA CCTCTCTCAA CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT     2460

TTCTTCCTCC TCATGAGGTC AGTTTTACTT TCTGCTGTTC CAGTATCGTT TTTCCTCGCT     2520

AGATTTCCTC AAAAGGGCAG ACTCCTCCCT TGGTGCGTCA CACGATTTTT TCATCTCGAC     2580

TGTTCTTTAA TGCATCATTA ACGACGCTTT TCTTCTAGGT GGTTCATAAG GAACAGGAAG     2640

ATTCAGGTTG ACTTTTCTAA TCCTAGAATA AAGTGCTGAA AACAATTCGG AATAGGCATA     2700

GAGACTAGAC AATTTGAGGA GCTGCTTGCG TCCTGTTCGA ACACATTTTC CCACCACGTG     2760

AAGA                                                                  2764
```

(2) INFORMATION FOR SEQ ID NO: 241:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1682 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```
CCGTTTTTTT CATTGTTCAG TACTACAACT TACGTTGTAG CGCCCTGCAC ATTGGTTCGT       60

CTTGTTCAGT TTTCAAAGGT CTTTGTCACT TGCTTCTCTC AAGCGACAAC TATATTAGTA      120

TATCACAACT GCTTTCGCTT GTCAACACTT TTTTGAAGAT TTTTAAGTTT TTTTAAACTT      180

TTTTTCATCA AGTGGTCCTG ACGCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT      240

TACCGCCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTTATTTTC      300

AACTCTTACT ATTATACAGT CTTTTCAAAC TTTGTCAACT ACTTTTTTAA ACTTTTTTTA      360

TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT      420

AATGAAGATC ATAGACTTCT ACTAAGCGTA CCAAATCACG AGCCAAGGTC GAAACATTAC      480

AAGAAATATA AACCATTTTT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTTATCAT      540

CCAGACCTGT ACGTGGTGGG TCAACAATCA AAGCATCTGC TCGGTAGCCT TCCTTGTACC      600

AACGAGGAAT AATCTCTTCT GCCGTTCCAG CTTCATAATG AGTATTGTCA AATCCCATTC      660

TTTTAGCATT TCGCTTGGCA TCTTCAATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG      720

TTTTTACTTT CTTTGCAAAG GCAAATCCAA TCGTTCCAAC TCCACAATAA GCGTCAATCA      780

AATGGTCTTC TTTATCAACA TCCAGCGCTT TTACTGCTTC GCTATAGAGG ACTTCTGTTT      840

GCTCAGGATT TAGTTGATAA AAAGCTCGAG GGGATAGTGA AAATTCATAA TTGAGTACAC      900
```

1263

```
CTTCTTGAAT ACTCTCTTGC CCCCAGATAA TCTCTGTCTT TTCACCATAT ATCTCACTGG       960

TTTTAGCTGT ATTTGTATTA ACAGCTACTG TCACAACTTC TGGGAAATCT TTAACCAACT      1020

CTTTTACCAA TTGAGTTAAA TTAAGCTGGC GGTTTGTAAC AATAATAATC TGAACCTGTC      1080

CGGTCTTTCT CGCGCGTCGG ACCATAATAG TACGGACACC TAGAACTTTT CTCTCATCCG      1140

TGATTGGAAT CTGGTGATAA GTAAGTAATT CTGCTAAGCG ATTAGCAATC ACTTGGGTTT      1200

CCTTATCTTG TACCAGGCAG TCTTTCAACT CTACTAAATA GTGAGAGTTT TGTGCATATA      1260

AGCCCGCCTT GACCTGATTT TTAAATTTTC GAGTCTGAAA TTGTAACTTA GCTCTGTAAT      1320

ATTTTGGTTC CTGCATTCCA ATAGTTGGAC GAATTTCATA ATTTTCATAT CCTGCAGGAG      1380

CAAATTTTTT CAGCGCTTGA TGAAGTAAGT CCGTCTTGAA CTCCAGCTGC TTATCATAAT      1440

GCAGGTGCAT GATTTGGCAG CCTCCGCATT CATTATAAAT AGTACAAGAT GGCACAATTC      1500

GAAATTTAGA CTTCTTGTTG ACCTTCAGTA ATTTTGCTTC AACAAAGTTG CGTCTAATAG      1560

AAGTAATCTG ACAATAGATA TCTTCGCCTT TGAGAGCTCC TGGTACAAAG ACTAATGTTT      1620

TTTGGTAAAA GCCGATTCCC TCACCGTTAA TTCCCATGCG CTTGATTTTT AATGGTATTT      1680

TT                                                                   1682
```

(2) INFORMATION FOR SEQ ID NO: 242:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2524 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```
TTAACTTTGG TCAATTCTTT AAAGTCATCC TCTGTAAGCA TGTCTAACCA TTGATGTTTC        60

CCTTTATTGC TAAAATCACC AATTCCGACT ACAGCTATAT CTAAATCTTT CCAACTATTT       120

TTCAAATTTT CAAAATATCT TGATTGCAAA ATACCATCTG CTAACAATTT ATTTTCTTGC       180

ACAATCGTTG CATTCATAAA TGTACACTCT CCATGAAATT TTCTAGACAT TTCATAAATC       240

AGTGTATTCA CATGGTATTT AGCGTGTATG TGACTAGGAC CACCTGCTAG AGGATAGAAG       300

TGAACATTTC GGACACTTTT ACTGTGAATT AAATCTACTA AATTACTTAA ACTTTTCCCC       360

CAAGAAAAGC CAATTTTCAT ATTATCATCA ATTAGATTCC TAAGGACGCC TGCTGCAACT       420

TGAGAAATTC TTTCAGATAA AATTGTTGGA GTATCATCAA ATTCATTTGG AATAATTTCT       480

AAACTTTCCA AACTGTATTT TTCTTTTACA TAATTTTCCA ACTTAAACAT ATTGGTATCA       540
```

1264

```
AAATTCTCTA TTTCAATTTT AACAATTCCT ACATTCCTTG CTTCTGTTAA CATTCTACTA      600

ATAGAGGTTC TATAAATTCC TAATTTTGCT GCTATTTGTG ACTGATTTAA GTTTTCAATA      660

TAATACAGAT AAGCAATTTT AGAAAGCAGT TTATTCCTAT CTTGATTCAT ACACTTAACC      720

TCTTACGAAA CTACCTTAAC CATTATCCCA GCATTTTCTA ATGTAGCTAT ATTTTGTTTA      780

GAAAGTTTTT CGTCTGTTAT TACTTCATAG ACTTGACTTA AAGCAAATCT TCTTACTGTA      840

CCTCTTTTAT CAAATTTACT TGAGTCAGTT AGGACAATGA CTTTATCCGA CACTGCTGAA      900

ATATATTGAA CTACCTCACT GCGCATTAAA TCTTTTCCGG TAAAGCCCAT CTCTTTATCG      960

TAACCATCTG TCCCAACAAA AGCTTGACAC ACATGAAAAG TCTGTATCAT TTCTTTTAAT     1020

AAAGGTCCTA CAGTCACCTG TGAATCTTTC TGAAACTCAC CACCAAGAAC AATAACACGA     1080

CATGAATCAT AAGCTCTCAC AAAATTTGCT ATAAAAAACG AATTTGTTAC AATCGTAACA     1140

TTTCTTTTTT GCTTGCAAAT TTCCTCAGCA AGTAAAGCAC AGGTCGATCC AGATTCTATC     1200

ATTATTGTTT CATTATCTGA CACCAATTTT ACTGCTTCCT GAACAATTTT TCTCTTAGTT     1260

TCATAATTAA TTGACAAACG TACATTTAAG TCATCTCCAC TATTTAATAC AGCATATCCA     1320

TGCTCTCTGT GTAATAAACC TTTTGACTCT AATTTATCTA AATCTTTTCT AATCGTTACT     1380

TTCGATACAT TTAATTTTTC CGATAATGTA TTAACGTCGA TCTTTTCATA TTCTGATACT     1440

AATTTAATAA TTTGTTCCAA TCTTTTCATT TTACACCTCC GTTTTATTCT ACCAAAATAA     1500

AAAGCAAAAA ACAACAAATT AACCTTTCGT TCGTAATTGT TTTTCTTTCG TTTTTGTGAT     1560

AGGATAGACT TATGAAGAGG AGGAACTCTT ATGGAAATAT CTAAAGGAAT TATTTTTAAT     1620

ATTCAACACT TTTCAATTCA TGACGGTCCG GGTATTCGTA CAACTGTTTT TTTAAAAGGA     1680

TGTCCTCTGC GCTGTCCATG GTGTTCTAAT CCTGAATCTC AAAGAATGAA ACCTGAAAAA     1740

ATGAAAGATG CTCAACGAGA GAAATTCACC TTAGTCGGTG AAGAAAGAC TGTAGAAGAA      1800

ATTATTACAG AGGTATTAAA AGACAAAGAA TTTTACGAAG AATCCGGTGG AGGTTTAACT     1860

TTATCAGGAG GTGAAATATT TGCTCAGTTT GAATTTGCTA AAGCCATCTT AAAATCAGCT     1920

AAAGAACATC ACATACACAC TGCCATTGAA ACTACTGCCT TTGTTGATCA TGAAAAATTT     1980

ATTGATTTAA TTCAATATGT GGATTTTATC TACACAGACC TAAAACATTA TAATTCTATA     2040

AAACATAAAA AAGTGACTGG GGTTTTTAAT CAAATGATTA TTAAAAACAT TCATTATGCT     2100

TTTTCACAAA ATAAAACTAT CGTTTTAAGA ATCCCAGTTA TTCCTAATTT TAACAATAGT     2160

TTAGAGGATG CAGAAAAATT CGCTACTCTA TTTAACTCAT TAAATATCGA CCAAGTTCAA     2220

CTACTCCCTT TTCATCAATT TGGTGAAAAC AAATATCGTT TATTAAATCG GAAATATGAA     2280

ATGGATGGAA TCAACGCACT TCATCCWGAA GATCTTATTG ATTATCAAAA GGTATTTCTG     2340
```

1265

```
AACCACCATA TTAATTGTTA TTTCTAGTTT ATTTCCTTGA AATGCTCTAG CTATTTGCAG      2400

ATAACAAGCA TCTATAATAC ATACTTAACT TTTCAAAAGG TTTAGCTAAA AAATTTTAGC      2460

CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTTAAAC TGCTATACTT ATCACAAAAA      2520

AACG                                                                    2524
```

(2) INFORMATION FOR SEQ ID NO: 243:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 2359 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```
CGTGCTTGGG GGCTTGTGGT CAAAAGGAAA GTCAGACAGG AAAGGGGATG AAAATTGTGA        60

CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGGTGACTTG AATGATGTTC       120

GGATGATTCA GTCAAGTAGT GGTATTCACT CCTTTGAACC TTCGGCAAAT GATATCGCAG       180

CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA       240

GTCTGGATCC AAATCTAAAA AAATCCAAAG TGAAGGTCTT AGAGGCTTCT GAGGGAATGA       300

CCTTGGAACG TGTCCCTGGA CTAGAGGATG TGGAAGCAGG GGATGGAGTT GATGAAAAAA       360

CGCTCTATGA CCCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA       420

TCGCTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAATGCGC       480

AAGCCTTTAT CAAAAAAGCT CAGGAATTGA CTAAGAAATT CCAACCAAAA TTTGAAAAAG       540

CGACTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTTG       600

GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCCTGAACA AGAACCAAGT CCACGACAAC       660

TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTTAA AACGATTTTT ACAGAAAGTA       720

ACGCTTCTTC AAAAGTAGCT GAAACTCTTG TCAAATCAAC AGGTGTGGGT CTTAAAACTC       780

TGAATCCTTT AGAGTCAGAC CCACAAAATG ACAAGACCTA TTTAGAAAAT CTTGAAGAAA       840

ATATGAGTAT TCTAGCAGAA GAATTAAAGT GAGGAAAGAA TGAAAATTAA TAAAAAATAT       900

CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTTTGTT CCTATGAGCT TGGACGTTAC       960

CAAGCTGGTC AGGATAAGAA AGAGTCTAAT CGAGTTGCTT ATATAGATGG TGATCAGGCT      1020

GGTCAAAAGG CAGAAAACTT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC      1080

GAACAAATTG TTATCAAGAT TACGGATCAA GGTTATGTGA CCTCTCATGG AGACCATTAT      1140
```

1266

```
CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA    1200

GATCCGAATT ATCAGTTGAA GGATTCAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC    1260

ATTAAGGTAA ACGGTAAATA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT    1320

CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA    1380

GCAGATAATG CTGTTGCTGC AGCCAGAGCC CAAGGACGTT ATACAACGGA TGATGGGTAT    1440

ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGGTGATG CTTATATCGT TCCTCACGGC    1500

GACCATTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA    1560

GCCTATTGGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAT    1620

CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA    1680

AATCAAGGGG AAAACATTTC AAGCCTTTTA CGTGAATTGT ATGCTAAACC CTTATCAGAA    1740

CGCCATGTGG AATCTGATGG CCTTATTTTC GACCCAGCGC AAATCACAAG TCGAACCGCC    1800

AGAGGTGTAG CTGTCCCTCA TGGTAACCAT TACCACTTTA TCCCTTATGA ACAAATGTCT    1860

GAATTGGAAA AACGAATTGC TCGTATTATT CCCCTTCGTT ATCGTTCAAA CCATTGGGTA    1920

CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG    1980

CAACCAGCTC CAAGCAATCC AATTGATGAG AAATTGGTCA AAGAAGCTGT TCGAAAAGTA    2040

GGCGATGGTT ATGTCTTTGA GGAGAATGGA GTTTCTCGTT ATATCCCAGC CAAGGATCTT    2100

TCAGCAGAAA CAGCAGCAGG CATTGATAGC AAACTGGCCA AGCAGGAAAG TTTATCTCAT    2160

AAGCTAGGAA CTAAGAAAAC TGACCTCCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT    2220

TATGACTTAC TAGCAAGAAT TCACCAAGAT TTACTTGATA ATAAAGGTCG ACAAGTTGAT    2280

TTTGAGGCTT TGGATAACCT GTTGGAACGA CTCAAGGATG TCTCAAGTGA TAAAGTCAAG    2340

TTAGTGGAAG ATATTCTTG                                                  2359
```

(2) INFORMATION FOR SEQ ID NO: 244:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1052 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```
TTCTTTCTGC TATAATCGTA TAAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTTAAA      60

TTTGGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTTAAA CATCGTCAAA     120

AGCGATTCAG AGCGTCGTTT TGTAGTCGTT TCTGCGCCTG GTAAACGCAA TGCTGAAGAT     180
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1267

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ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCGCGACT ATGTTGCGGG TAACGATATT        240

AGCAAGAACC AAAGCTGGAT TATCGACCGC TATGCTGCTA TGGTTAGTGA ATTGGGACTA        300

AAACCAGCTG TGCTAGAAAA AATTTCTAAA AGCATTCACG CCTTGGCCAC TCTTCCTATT        360

GAAGAAAATG AATTTCTCTA CGATACTTTC CTAGCAGCCG GTGAAAATAA CAATGCCAAA        420

TTGATTGCTG CCTACTTTAA CCAAAATGGT ATCGATGCAC GCTATATGCA CCCTAGAGAA        480

GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCGCA TCATTCCATC AAGTTATGAC        540

AAGATTGAAG AATTGACAAA CACCAATGAA GTCCTTGTCA TTCCTGGTTT CTTTGGTGTC        600

ACTAAGGAAA ATCAAATCTG TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC        660

ATTGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACTTTA CGGACGTTGA TGGTATCTTT        720

GCAGCCCACC CTGGTATTAT CCACCAACCA CACTCGATTC CTGAGTTGAC CTACCGTGAA        780

ATGCGCGAGT TGGCCTATGC AGGCTTCTCA GTCCTTCATG ACGAGGCTCT TCTTCCTGCC        840

TACCGTGGAA AAATTCCTCT GGTTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT        900

CGTATCGTTC TAAAACACAG TAATGATGAA TTTCCAGTTG TGGGAATTGC TGGTGACTCA        960

GGCTTTGTCA GCATTAACAT GTCGAAATAC CTCATGAACC GTGAGGTTGG ATTTGGCCGC       1020

AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT                                      1052
```

(2) INFORMATION FOR SEQ ID NO: 245:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 855 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```
CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTCGTGA CTGGTGGGAA         60

AATCGTGAAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTTAC ACCTAGTGAA        120

TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC        180

TTAAATCCCT TTGAGTTGAT TCAGAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG        240

ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAAATAATG ACACCAGAAC        300

AACTTAAAGC AAGTATTCTC CAAAGAGCGA TGGAAGGGAA ATTAGTGCCG CAAAATCCCA        360

ATGACGAACC TGCAAGTGAA TTATTAAAGA GAATTAAAGC TGAAAAAGAA AAACTTATCA        420

GTGAAGGAAA AATCAAACGA GATAAAAAGG AAACTGAGAT ATTTCGTGGT GATGATGGGA        480
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1268

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AACATTATGG GAAGTTTGCT GATGGAAGCA CTCAAGAAAT TGATGTTCCT TATGATATTC        540

CTGATACTTG GGAGTGGGTG AGGATAAAAT CAATTTATTG GAATTTTGGG CAAAATAAGC        600

CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAAG AACATAATCA        660

ACTACAAAAA TCTACAATAT CTTTCACCTG AACAAGCGCC TTCCCGTGCT AGAAAATTAG        720

TTTCGCAGAA TAGTGTCTTA TTTTCAACAG TTAGACCATA TCTAAAAAAT ATTGCTGTAG        780

TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTTG GGATACTTTA        840

CTTAACGAAA CATAT                                                        855
```

(2) INFORMATION FOR SEQ ID NO: 246:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 660 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```
TTTAGGAAGG CTATCCGTAA TTTTACAAAG GATTTAGATA TTACAGAGGA ACATTTAGAT         60

ATTATCAAAA GAGAGATGTT TGGCGAATTT TTCAGTAGCA TGAACTCTCT TGAATTTATT        120

GCAACGCAAT ATGATGCTTT TGAAAATGGT GAGATAATTT TTGATTTGCC GAAAATTTTA        180

CAGGAAATTA CTTTAGAGGA TGTCCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC        240

ATAGTTGATT TTACAATATT CCCATCGTAG TAACCTATTA TAATAGACAC TAGAAAGAAG        300

GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC        360

AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG        420

CAATGGAAGC AGACGATTTC GATCAACTTC CAAGTCCTTT TTACACGCGT TCTTTCTTGA        480

AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTTGGATGCT TATGATTCTG        540

GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTCGTAGAC        600

GTTCAAGTAA GAAAAAGAAG AAAAAAACAT CATTTTTACC TTTATTTTAT TTTATCCTGG        660
```

(2) INFORMATION FOR SEQ ID NO: 247:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1805 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

1269

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CCGGTTGCAC AGGATCGTGC ATAGTCAACT CTTCAAGTAT AGCATATCTC CTATTTTCTT        60

ACAAGTAATA ACACCTAAAA TGAAGCTTTT TCTTTTACTT TTTTCTGCCA AGAGGCAAAA       120

AGCATGCTGA GGTAAAAAAC GCTCATCATA ATAGGAACAC CAAGAATGGT CTTTTCATGA       180

TAGAAAATCG TCAAATAGGC TGAAAAGACA ACGCCAAGGA CAAAACTACT AAGCAGGCTA       240

ACAAATATGA ATCCTTCACG CAAAAAAGGA GTGTGCTTGG TTCGGAAATA ATCTCCAAAA       300

GCCAGCATGG TCCGTTTGAT ATTCCCTGTC ATAAAAGCGT TATTATAGGC AATACCCGAC       360

ACTTCTCCAA AAGCAGTTGT CACCAGTCCC ATACAGAAGG CCAAGGGCGG CACTAGATAG       420

ATATTATCCA CAGTTTGCGG CACAAAAGCA ATAATGATTG ATAAGATTGC CAAGGGAATC       480

AAGGACAGAA TAGGTTTTTT CACAATTCTC AATTTTTCCT TATAAATCGT TAATAAAAAG       540

ACTCCCATCA TAAACGCTAG CAAGGTGAGA ACCTTGTCCC TAACATCCGA AACATTATTT       600

TTAATTAATT CTACTGAAAG AAAGACAACA TTTCCAGTTT GTCCAGCTAC AAGGGTATTC       660

CCGCGAACAA TAAAAGTGTA AGCATCCACA TATCCAGCAC AAAACGTCAA AAAAAGTGCT       720

AACCTTTTAG ACTGACGTGA TATTTTTCTT ATAGGTAATA ACCTCATTTT ACCTCCCATT       780

GTATTTCTC TTAGAAATAT TGTACCATTT TCTTTCTAAA AAATCGTAGG CTACCATTTA       840

GATTTTACTA TTAGCATAAA AATAATAATA GACAACTATT TATCCAAAAA TAGATAGATG       900

TAACATGTTT GCAAACAAAG CATACGAACC TTTAGTAAAA TCATTCCAT GAAACTAGAA       960

TAGAGCCCTC TTAGCAAAAA TCATTATTTT AATTTATTTC TAATCACTCC TTGACATAAA      1020

TAACTCTCAC CAATAAAAGA CTATGTCTTA AAAAAATGGT ATAATAAAAT CAATACTTGG      1080

GCTTGATGGC TATGCTACTA ATAACAATTA GGAGAGAAAA TCAGGCACTT GTTAACAACA      1140

AGGATTATCC CCTTGAGATG AAAGGAACTT TAGAAATCTT ATGATGAACA TGCAAAACAT      1200

GATGCGTCAA GCACAAAAAC TTCAAAAACA AATGGAACAA AGCCAAGCTG AACTTGCTGC      1260

TATGCAATTT GTTGGCAAAT CTGCTCAAGA TCTTGTCCAA GCGACCTTAA CTGGCGATAA      1320

GAAAGTTGTC AGCATTGATT TCAATCCAGC TGTCGTTGAC CCAGAGGACC TTGAGACTCT      1380

TTCTGATATG ACCGTTCAAG CCATCAACTC TGCTCTTGAA CAAATCGATG AAACTACCAA      1440

GAAAAAACTG GGTGCTTTCG CTGGGAAATT ACCTTTCTAA AAACAAGGAG CTAGAACAAT      1500

GCTTGTCGAT AACAAAGGCT AAGAAAGGTG CAAAAATGAC TCTATAATAT TTGTAGTGGG      1560

TAAATCCCCT ATGGATATTA TGGAGCCTAT TTTTGTGTAG AAAAAAGTCC CATATGACCT      1620

ATAATGAAAA GCGACAAAAC AACTCATTAG AAAGAATCAT ATGGAACAAT TACATTTTAT      1680

CACAAAATTA CTAGACATTA AAGACCCTAA TATCCAGATT TTAGACATCG TCAATAAGGA      1740
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                                    1270
TACACACAAG GwAATCATCG CCAAACTGGr CTATGAAGCT CCATCTTGTC CTGAGTGCGG      1800

AAGTC                                                                 1805
```

(2) INFORMATION FOR SEQ ID NO: 248:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2516 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```
CTGCATCTAG TTTGTTTCTC CCTACAGTTT TAGCTAGACA GATTGGAGAT TATGATTTAA       60

CGTCGCCGCG TTGGGGTTCG GATACAACTA GTGAGCTTGA GAAAGAAAAC TCCTCTGCTG      120

GAATTAATAA TAATGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCGTAGCG      180

CCTATAGTGG GTCAGATATT ACCCCGGTAT ATTCATTGGG GTCTGGCTCT AGGATTGTCA      240

TGTACTATAA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC      300

CACAATTTGG AAATCATGTA AGAATTCATA CTTCAGGTTC TTGGAATCCA GATTCTTATT      360

AACTTACTTG TCAGAGTAAG CCTTAAAGAT GGTTGATTGT GGGTGTAGCA TGAAAAAAGA      420

ATGCTACACC CTATTTTTAT TATAAGGAGG AGTAAGGATG GAATTTTTCA TTTGTAATCT      480

TGTACGAGTC GTTCAATCAC CTCGATTTTA TATGTCTTTA TTTTTGACCC TTCTTTGCAT      540

GAGTTTAGGA AATTTCCTTG CTTTCAATGG TATTTATAAA ATTGAAGGTT TATCGATTTT      600

TTTTGCCGCT TCTTCTATTC GAGGATTTTC ACCGATTAGC CTAGTAGCTG CACTTATCTG      660

TACACTGCCC TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGCACA      720

ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTC      780

TTCTTTTCTA GTCTTTTTTC TCCCCTATTT ATTATTATTA GGAATTAATC TTTTAGTGAC      840

TCCTTATCAG GAAATTTATA TTGGAGATTA TAGTGGTGCC TTAAAAGAAT TATTTGATTC      900

CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG GCGCTGTGTT      960

CTCTATTTTT GGACTAGCTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT     1020

CCCAGTTGCC TATATGATGG TTGGTGGTAT TTTTTGGGCT ATTTTAGGGC TATCTTACTT     1080

AGAACCTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCTTT CCTTAGTTAG     1140

TGCTCATCTT GCTTTTATTT TATTTGTTAG TTGTTTGGTT GTTTATGGTA CATTTTTTCT     1200

ACATTCAGAG GACTATGTAT AATGAAACAA TTTGTTCAAT TTTATAAAAA AGATTCTTA      1260

GCAGTATTGG TTTATTTTAT ATTACTGCTA TCCTGTGTTT TATCTAGTAC AGTATATTTA     1320
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1271

| TTGCGCtGTC | GCCAATATTC | AATCCATCCA | AATGTATTAG | AATGGATCTT | AGTTTTACTT | 1380 |

CAAGATATGA CGACTGGAGT ATATTGCTTT CCGTTCACAT ATATATTGTT CTTTTTTTAT   1440

TTGATGAATA ACTATTTTAA TAGGTTGGAG TGTCGCATTC GTCTGAAATC AATTAAGCAC   1500

TTTACCAGTT TTAGTTTCAA ATTAGCAGCT CTTAGTACGG GGATTTGGAC GGCGACTTTA   1560

TTTTTATTGA TTTTTCTAAT TGCATTTAGT AATGGTTTTA GCTTCTCTTT GGAGATAAAG   1620

GAGGTTGATT TTTTAAGAGA ATTTTATGGT ATAAGTATTG CAAACAATGC TAGTTTCTTT   1680

ATAGGATTTT TTTTCTCTTA TATAGCATAC TATTTCTTTT TATCCTTACT TACTATTAGC   1740

AGTTTTTCTT GGTTTAAAAA ATCAAACATG AGCTTAGTAT TTCTGTTTAC TTTTTTATTT   1800

GTAGAATCCT TATTCTGGAT TTATCAGTTG GACAATGGGA TAATTGGATT ATTGCCAATT   1860

TTTCAGTATA TGGTAAATTC CAATCCGTAT GCATTGATTT ATTGGCTTAC ATTACTATCT   1920

ATCATAATTC CATTGACTGT ATTTTCTGTT CATAGAAACT GGAGGAGAGT GTAAAAGTTG   1980

GAAATGGGAA AGTTAAGTAG TCACATGTGG AGGTTGAATC AGATAATCTA TACCAAGTAC   2040

TTTTGGGGTT ATGTTCTTTT TTGGATATTG ATTTGTTTAG GATTATGGTA TTGGTTAGAA   2100

GGAAATGATA GACTTGTTAT AGAAATTTTA AAAGGGCCTA ATCTGAGTCA AAACTCTTTT   2160

TTAGTCTTAT CTATATGGTT GCTTCATTGG TTTATTATTC ATACATTTTT TCTAGCAGTT   2220

GTATATCGTA GAAGAGCATC CGATTTCTTT ATGGAAGTGA TTCGATTTTC TTCTATTAAG   2280

CTCTGGATTA GGTATCAGAT TTGGACCTGT TTTCTTTATG GACTCATTTT AATCATGGTA   2340

AAAGTTCTAG TGATTCAATT TATGTTACAG TTACCAAACT GGGATATAGG AGTTTTGTTT   2400

ATAGTTGATT CTTTGAATGC TTGTGTGTTA GTCTTGTTTT GCTTTATGTT ATACGCACTA   2460

GGAGCGAATG TACAAATGAA CTTTGCTTGC GTTAGTTTCT TTTTACTCAT GATTGG   2516

(2) INFORMATION FOR SEQ ID NO: 249:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1364 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTTT TTGTAAATTT TCTAGCACTT GTATGGTAAA ATAGATACAG GTGTTCATTA   60

AACTAGACTA AAAACCTATT TAAGCAGGCA AAATGAAGAA ATACCAACAA TTATTTAAGC   120

AAATCCAAGA AACCATTCAA AACGAGACTT ACGCTGTCGG AGATTCCTT CCTAGCGAGC   180

1272

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ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGcCC TGTCTCTCCT      240

CCAAGAGGAA GGATTGATCA AAAAGATAAG AGGGCAAGGT TCTCAAGTCG TCAAAGAAGA      300

AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAACTAGTTA AAGAACTTGG      360

ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC      420

ACTGATAACC GGTTTCCCAG AGTTTCGGAT GGTTTGGAAG GTGGTCCGCC AGCGTGTGGT      480

GGATGATCTG GTATCCGTTC TGGATACGGA CTATCTGGAT ATGGAACTCA TCCCAAATCT      540

CACTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAATGGCC TCAAACTCCT      600

TATTGATTAT GCTCAGAAGG AAATCACCAT TGACCACTCA AGCGACCGAG ACAAGATTCT      660

CATGGACATT GGCAAAGACC CTTATGTCGT TTCGATTAAA TCAAAAGTCT ATCTCCAAGA      720

CGGACGCCAA TTTCAGTTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTTGTAGA      780

TTTTGCAAAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTCAGCCTTT TTCGGCTCTA      840

TAATATTTGT AGTGGGTAAC CCCCCTATGG ATATTATGGA GCCTATTTTG TGTAGAAAAA      900

AAGTCCCATA TGACCTATAA TGAAAAGCGA CAAAACAACT CATTAGAAAG ATTCATATGG      960

AACAATTACA TTTTATCACA AAACTGCTCG ATATTAAAGA CCCAAACATC AAGATTCTAG     1020

ACATCATCAA TATGGATACC CACAAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT     1080

CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC     1140

CTTACCTCGA AACAACTGGT ATGCCTACTA GAATTCTCCT TAGAAAGCGT CGTTTCAAGT     1200

GCTATCATTG TTCTAAAATG ATGGTCGCTG AAACTTCTAT CGTCAAGAAG AATCATCAAA     1260

TTCCTCGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAGATT TCTATGACCG     1320

ATATTGCTCA TCAGCTGGCC ATTTCAACTT CAACTGTCAT TCGG                     1364
```

(2) INFORMATION FOR SEQ ID NO: 250:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1227 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```
CCATGAAGAC CGCTTGGAAT TGGAATGGCA CAAGTCTTTG TTGAATGGTC TATTCCCATT       60

GACAATCGGT GGAGGAATTG GACAATCTCG TATGGCCATG TTCCTACTTC GCAAGAGACA      120

CATCGGAGAA GTGCAAACAA GTGTTTGGCC TCAAGAAGTC CGCGATACTT ACGAAAATAT      180

TTTGTAGAGA ATCGAACCGC AAGGTTCGGT TTTCTTTCTC TTTTTGTCTA TAATTTGGTA      240
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1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACGTCCCCTC AAGACACTAG   300

AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTTAGGGG AGCCATTTTT AACATGATTG   360

GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTTTATCTA   420

TCGAAGCAGT ATCGCGTGGC ATGTCCAGTG CTGTTTTGGT GGAGCGAGAC CGTAAGcTCA   480

GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTTC AACTCCTCAA   540

GATGGATGCA GAAAGGGCAT TGGAACAGGT ATCTGGGGAA TTTGACCTCG TTTTCTTAGA   600

CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT   660

TTTTTCTGAA GATGTTATGG TTGTGTGCGA GACGGATAAA GCCGTTGAAC TTCCAGAAGA   720

AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTTATGGA ATTAGTAAGG TGACAGTCTA   780

TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTTGATCC GATGACAAAT GGGCATCTGG   840

ATATCATTGA ACGGGCGAGC AGACTTTTTG ATAAGCTTTA TGTGGGTATT TTTTTTAATC   900

CCCACAAACA AGGATTTCTC CCTCTTGAAA ATCGTAAACG GGGGTTAGAA AAGGCTGTGA   960

AACATTTGGG AAATGTTAAA GTCGTGTCTT CTCATGATAA ATTGGTGGTC GATGTCGCAA   1020

AAAGACTGGG GGCTACTTGC CTAGTGCGAG GTTTGAGAAA TGCGTCGGAT TTGCAATATG   1080

AAGCCAGTTT TGATTACTAC AATCATCAGC TGTCTTCTGA TATAGAGACT ATTTATTTAC   1140

ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTTG   1200

GTCAGGATAT TGCCTGCTAT GTTCCCG   1227

(2) INFORMATION FOR SEQ ID NO: 251:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 3652 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAACGCT ATTTCTTCCC ATTTTATTTA TTTTTTAGGA GTGGTAACGT   60

ATCAAAATAG CCCAAGCGTT CTCACCCGTG TGAGTTTGAA TAATGGAACC CGTTTCCAAA   120

ACAGAAATTG GCTTTTCAAC ATAAGCTTGT AAGCTTTCTT TCATCTCTTT TGCCCAATCA   180

TCACTACCAG AATATGAAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAG CGATGTTATC   240

AACTCATCTA ACCATTTTTT AAATGTTTTA GTTCCACGAC CTTTAACCAT TGGCTGCAAT   300

TCATGGTCTT TCATTTGCAT GACAGCACGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT   360

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                                    1274
ACACGGCTAA TTCGTCCACC TTTGACAAGA TTTTCCAAAG TTGAAACACC AATATAAAGC        420

TCTGTATGGT TTTTAACCTC TTCTACATGA GATAAAATTG CCTCCATATC TTTACCTTCT        480

TGAGCTAACT TCGCAGCCTC AACAACTTGG AATTTCAGGG CTTGGTCAGT GAAGGAACTA        540

TCAACAACAG TCACATCTGC AGTAGATAGG CTAGCACCTT GGCGTGCTGC TTCTACCGTA        600

CCCGAAAGAG CATGGGACAT ATGAATAGCA AGAATCTGGC CACCATCTTT GCATAGGTCT        660

TCAAAAATCT CAGCAAAGAC ACCTACAGGT GGCTGACTTG TTTTCGGAAG ATTCTTACTT        720

TCTTGCATCA ACTGAAGAAA TTTACCTTCT TCTTTCAAAT CCGCATCAGA ATAAACAACA        780

TTATCAATCA TTACAGATAA TGGAACAATT GTAATATCTA ATTGCTTTAC TAGTTCAGGT        840

TCAATAGTAA CAGATGAATC GGTTACAATC TTAATTTTTG TCATAGTATC AATCTTTCTA        900

TTTTAGGATT CAGATTGGTT TCCTTACTTC TAATTATATC AAAAAAAAGA TTAAAAATCC        960

TAATGGAGTC AATCAAATTT TCCGTAAAAT TTGATATAAT CAACTTATAA GAAAAGAGGT       1020

GTCCTATGAT TAAAAAAATT TACCCCATTT TTACCATTTT ACTAGGTGCT GCTATTTATG       1080

CTTTTGGACT GACTTATTTT GTAGTTCCCC ATCATCTCTT TGAAGGAGGG GCGACAGGCA       1140

TTACCCTCAT CACCTTTTAT CTTTTTAAAA TCCCTGTTTC CCTCATGAAC CTGCTGATTA       1200

ATATTCCCCT TTTCATCCTA GCTTGGAAGA TTTTTGGAGC CAAATCCCTC TATTCTAGTT       1260

TACTAGGAAC CTTAGCTTTG TCCGGCTGGT TAGCTTTTTT TGAGCATATT CCCCTTCATA       1320

TTGATCTTCA AGGTGATTTA CTAATCACAG CCCTTATAGC GGGAATCCTA TTGGGAATTG       1380

GCCTTGGAAT TATTTTTAAT GCTGGAGGTA CAACTGGCGG AACTGATATT CTAGCTCGTA       1440

TTCTCAACAA ATACACTCAT ATATCCATAG GAAAACTGCT CTTTATCTTA GATTTTTGTA       1500

TTCTCATGTT GATTCTCCTA ATCTTCAAGG ATTTGAGATT GGTTTCCTAC ACGCTTTTGT       1560

TTGATTTTAT TGTTTCTCGT GTTATTGATT TGATTGGTGA AGGAGGATAT GCCGGCAAAG       1620

GCTTTATGAT TATCACAAAA CGTCCTGACC AACTTGCTAA GGCGATTAAT GATGACCTCG       1680

GAAGAGGTGT TACTTTTATT TCTGGTCAAG GCTACTATAG TAAAGAAAAT TTGAAAATCA       1740

TCTACTGTAT TGTCGGAAGA AATGAAATTG TGAAAACGAA GGAAATGATT CATCGAATCG       1800

ATCCTCAAGC CTTTATAACT ATTACAGAAG CCCATGAAAT CCTAGGAGAA GGCTTCACCT       1860

TTGAAAAAGA ATAAAAAGAG GTAATGTCGT GACCTCAAAA GTTAGACTAA ATCATCTATC       1920

TTTTGGGTTA CAGACAACCT CTTTTTTATT TTATTTACTC AAGCTCTTAA GACCAATTCC       1980

GAGTTACTTC TTCATCAGCC TTTAACTGAT CCACTAATTG GTCAACTGAG TCAAATTTGG       2040

TCATATCTCG AATGCGATCA AGCCAATAAA CCATGACGGT TTCCCCATAA ATATCTTGAT       2100

TAAAATCAAA AATATTGACT TCAAAACGTG CTTCTTCTCC ATCAAAGGTC ACATTTTTCC       2160
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1275

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CGACACTAGC CATAGCACGA TACTTCTGTC TTTGAATCTC AACATCAACA ACATAAACGC       2220

CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACTAAATT CGCTGTCGGA TAACCAATTG       2280

TACGACCACG AGCATTACCA TGAACCACCA TACCTCTTGA TGGAAGCGGT GCCCCCAAAA       2340

GTTTTCCTGC TTCTTTCACA TTTCCATCTA AAATAGCTTG ACGGATACGA GTTGAACTAA       2400

TCTTTCCTTT CTCATCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT       2460

TTAAATCTTC TGCTGTTTTT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA       2520

TTTTGGCATT CATAGCCTTG ATATAAGTTG CAAAGAATTC TTGTGCAGTG AGACTAGCGA       2580

ATTGACTACT AAAATCAAGG AGATATAATT CTTCTACACC TTCGCGCTTT AATTTTCTTT       2640

CACGTTCAGC AGGGTTCAAA ATATGCAAAA ACAAATCTGG ATGATAAGGC TCTAAAGCGA       2700

TCTTTGGAGA TTCATTAAAG GTCATAACGA CGATAGGCAA CAAATCCTTT CTCGCAGCCT       2760

TGTTGGCAAC ACGAAATAAT TCTTGATGCC CCTTATGTAT GCCATCAAAA TAGCCGAGAA       2820

CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTTTGGTT TTTTATAGGA ATAGTAATAA       2880

TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAATCT GAAATGTTGT       2940

TTTTTTCACA TGAAGTGTAC CTGTTTTCAA AAAGCACTTT ATTCTATCGT TGCTTAACTA       3000

TGAACTTTGC AATATTCTTC TCAAAAACTT GTAGGACATC TTCAAAATTT TGCAAGGAGT       3060

GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG       3120

CAACTAACTC CTGAGAACTT TAAATTACTA ATTGGTGCCG AAAAGGTAGA ATTTAGAATC       3180

GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTTGGGCAAG ATGTTTGAAG       3240

AATTTCCTAA ACTCCCTGAT TTGAAGCAAG TCACTTTCCC TAATGACAAA GAAAAAAGCC       3300

AAAACAGCAA AGAAAAACTA GATGACTGCT TTCCAACAAC TCCCATCTAG TGTGCTTCAG       3360

ACTGGGCTAT TTTTCTCTCC ATCTGTTAGC TTGGATTCTC AGACCGTTTC AGCTAAAGAA       3420

TATCTTTTCC CTTATCGAAA GGAACGGCTC AAGCCATTCA GACAAGTGAA GGGACGACAA       3480

GCCAATATTT GAAACCAGAT AGCAGTTCTT ATAGTCAATT GAAATAAAAT CTGAAGAAAT       3540

CGAGTAGGAA ACTCATATCA ATGTTTAACA GTGTTCTATT CCAGATTCAT ACTCAATGAw       3600

AATTAAAGTG CAAACTAGGA AGTTAGCCGC AGGTGATACT TTGGGTACGG CA               3652
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(2) INFORMATION FOR SEQ ID NO: 252:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 743 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

1276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```
GTACCGTGGT GCCAAAGTAC AGCAAGGTTG GCTTTTTGAC AAACAATACC AATCTTGGTT        60

TTACATCAAA GAAAATGGAA ACTATGCTGA TAAAGAATCG ATTTTCGAGA ATGGTCACTA       120

TTATTATCTA AAATCCGGTG GCTACATGGC AGCCAATGAA TGGATTTGGG ATAAGGAATC       180

TTGGTTTTAT CTCAAATTTG ATGGGAAAAT GGCTGAAAAA GAATGGGTCT ACGATTCTCA       240

TAGTCAAGCT TGGTACTACT TCAAATCCGG TGGTTACATG ACAGCCAATG AATGGATTTG       300

GGATAAGGAA TCTTGGTTTT ATCTCAAATC TGATGGGAAA ATAGCTGAAA AAGAATGGGT       360

CTACGATTCT CATAGTCAAG CTTGGTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA       420

TGAATGGATT TGGGATAAGG AATCTTGGTT TTACCTCAAA TCTGATGGGA AAATAGCTGA       480

AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTTCAAAT CTGGTGGCTA       540

CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGGA AGCGATGGTA AATGGCTTGG       600

AGGAAAAACT ACAAATGAAA ATGCTGCTTA CTATCAAGTA GTGCCTGTTA CAGCCAATGT       660

TTATGATTCA GATGGTGAAA AGCTTTCCTA TATATCGCAA AGTAGTGTCG TATGGCTAGA       720

TAAGGATAGA AAAAGTGATG ACA                                            743
```

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4010 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```
TTTTGGTTGA TGATACGAGG GATTTGGTGA TTCTTCTTGA CGATAGAAGT TTCAGCGACC        60

ATCATTTTTG AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAGAAT TCTAGTAGGC       120

ATACCAGTCG TTTCAAGATA AGGAATTTTA GAAGGTTTTT GAAAGTCATA TTTCTTCAAT       180

TGGTTTCCGC ACTCAGGGCA AGATGGGGCG TCGTAGTCCA GTTTGGCGAT GATTTCCTTG       240

TGTGTATCCT TATTGATGAT GTCTAAAATC TGGATATTAG GGTCTTTAAT GTCTAGTAAT       300

TTTGTGATAA AATGTAATTG TTCCATATGA TTCTTTCTAA TGAGTTGTTT TGTCGCTTTT       360

CATTATAGGT CATATGGGAC TTTTTTTCTA CAATAAAATA GGCTCCATAA TATCTATAGT       420

GGATTTACCC ACTACAAATA TTATAGAACC GAATTAATTT AATTAGAGAG CCAACTTTCT       480

AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATACTA       540
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1277

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TTAGTAAAGT AAAACTATTG GAGGATATTT TAATGCCACA ACCTATTGTT CCTGTAGAGA          600

TTCCACAATC TCGTCGTTTT GATTCTAAAA AGAGAAATGA TATTCTGCTT AAAATTCGTA          660

TTGGCAAGCT TGAAGTAAGT TTTTTTCAAT CTCTCAATCT CGAAATGGTA GAACAGCTTT          720

TGGATAAAGT GTTGCTCTAT GACAATTCAT CTATCTAGCC TAGGGCAGGT CTATCTCGTA          780

TGTGGGAAAA CGGATATGAG GCAAGGCATT GATTCATTGG CTTATCTGGT TAAAACCCAC          840

TTTGAATTAG ATCCTTTCTC CGGTCAAGTT TTTCTCTTTT GTGGTGGACG TAAAGACCGC          900

TTTAAAGCCC TTTACTGGGA TGGTCAAGGA TTTTGGCTAC TATATAAACG CTTTGAGAAC          960

GGAAAACTGA CTTGGCCCAG TACAGAAAAG GATGTCAAAG CTCTCACACC TGAACAAGTA         1020

GATTGGCTTA TGAAGGGCTT TTCTATCACT CCAAAAATAA ATTTATCAGA AAGTCGTGAT         1080

TTCTATTGAA ATGAGGACTT TCTTTTTAGT TATAATAAAG TTAGGAAATA AGGAGAGGAA         1140

GCCCATGGAA GAAGATTGAA AATCATTCAA CAACAGAGTG CTACAATTGA TAGTCTCACC         1200

AATGAACTTG CCCTTCTTCG TGAACAAGTG GCTTATCTAA CGCAAAAGCT CTATGGAAAA         1260

TCCTCTGAGA AAAGTGTTTG CCCATCTGGA CAACTCAGTC TTTTTGAAGA GGAACAAAAT         1320

ATGGAAGAAG ACTCTGACTT ACCCAGTTGA AAGAGAAGAA ATCACCTATA AACGTAAGAA         1380

AGCTAAAGGG AAACGTCAAG CTCTTCTTGC CCAATTTGAT TCAGAAGAAG TTCATCATCA         1440

AGTAGAAGAG AGCATTTGCC CTGATTGTCA GGGAGATCTA AAAGAGATTG GAGCAACCCT         1500

TCAACGACAA GAATTAGTCT TTATTCCTGC GCAATTAAAA CGAATAGATC ATATCCAACA         1560

CGCTTATAAG TGCCAAGCAT GCAGTGATAA AAATCCGAGT GATAAAATCG TGAAAGCTCC         1620

TATTCCTAAA GCCCCTTTGG CGCATAGCCT TGGCTCAGCT TCTATTATCG CTCACACCAT         1680

CCATCAGAAG TTTAATCTGA AGGTACCCAA TTATCGCCAA GAAGAAGATT GGGCTAAGAT         1740

GGGTTTACCA ATCACACGTA AGGAAATTGC TAATTGGCAT ATCAAGGCGA GTCAATACTA         1800

TTTGGAGCCC CTTTATAATC TTTTACGAGA AAAGTTGTTA GAACAAGCTC TTCTTCATGC         1860

GGATGAAACC TCTTATCGGG TTCTAGAGAG TGATAGTCAG TTGCCTTACT ATTGGACTTT         1920

TTTGTCTGGG AAAGCTGAGA ATCAAGCAAT CACGCTGTAC CACCATGATC AGCGTCGGAG         1980

TGGTTTAGTA GTACAAGAAT TCCTAGGAGA TTATTCTGGC TATGTTCATT GTGACATGTT         2040

GCGGCAGTAA CTTAGGACTT TAGTCCTCTA GTTCTGCCTA TGCGATAGCA GTCCAAGGTT         2100

TAGGAGTAAG GCGACGCTAA GCTTGGTAAA CTGCGAACAG CTAGAAGCTT ATCGTCAACT         2160

GGAAGAAGCT GCACTTGTTG GATGTTGGGC GCATGTGAGA AGGAAGTTTT TTGAAGTGCC         2220

CCCCAAGCAA GCAGATAAAT CATCCTTAGG AGCTAAAGGT TTAGCTTATT GTGATCAGTT         2280
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                                 1278
ATTTTCCTTG GAAAGAGACT GGGAGGCTTT GCCAGCTGAT GAACGACTAC AGAAACGTCA      2340

AGAACATCTC CAGCCCCTAA TGGAAGACTT CTTTGCTTGG TGCCGCCGTC AGTCAGTTTT      2400

AGCAGGTTCA AAACTAGGAA GGGCAATTGA ATACAGCCTC AAGTATGAAG AAACCTTTAA      2460

GACTATTTTG AAAGACGGAC ATCTGGTCCT TTCCAATAAT CTAGCTGAAC GCGCCATTAA      2520

ATCATTGGTT ATGGGACGGA GTAAAAGAGT CCAGTGGACT CTTTTAGCCT GAGCTCAGTT      2580

TAAAAAAGCG AGGGTGGTTA TTTTCTCAAA GTTTTGAAGG AGCTAAAGCA AGAGCTATTG      2640

TTATGAGCTT GTTGGAAACA GCTAAACGTC ATCAATTATA GTGCGTTGAA TCTATAACAG      2700

TACGCATCGA CTGCTAAAAC ATTTCTATAA ATCAATTTTC CTTTCCTAAT CGATTTGTTC      2760

ATATCTTATT TCAATCCATT ATAAATAGCG AGAAATATCT ATCCTATCTT CTAGAATGTC      2820

TTCCAAACGA GGAAACTCTC GTAAACAAAG AGGTTTTAGA GGCCTATTTA CCGTGGACTA      2880

AAGTTGTACA AGAAAAGTGC AAATAAGAAA TCTCCAGATT AGGAACTATC CGTGAGTTCT      2940

CTAGTCTGGA GATTTTTCAA TAGACTTCGT TATTGGACGG TTACAATTTA TTATATGAAA      3000

ATCCCATATT ATTCTCCAAT TCTATATTTT ACCTTTCTAA ATGTATAGAT TAACTACCTA      3060

ATTATAGCAT ATAACGCAGA TTCCTTTCAA TCGTATGATT TACTGCATTA AATTAAGTAA      3120

AAAAATAAAG GCAGTCCGAA GACTGCCGAT ATTTATCTCT CATCTCTTTA ATTATGGTAA      3180

GTAAATAAAT AATTTCCCTA AAGATATGGA AATTATTAAT ACTATAAATA CATATTATAA      3240

AGTTTATAAA TACTGTAAAA ATCCTGAAGT TAATTTTCTA ATAAATATCA ATATGTGTTA      3300

GTATCTTTTA AATTTTTAGA CAATTTACTA GTTCTATAGA CATGTTTAAC AGACTCTATT      3360

TTACAATTCA AAAATTTCAT CTGCCACTTC ATTTAAAAAT TCTATATCAT GGGAAACAAT      3420

AAAAATTATT TTATCCATGG TTTTATACTT ATTAATCAGT TCAGATATTT TTATCATATT      3480

GGAATAATCC ATACCACTTG AAGGTTCGTC AAAAAAGACA AATGGAGAAT TCTTGCACAT      3540

AACAGATGCT ATTGCAAGCC TTTGCTTTTG CCCTCCTGAT AAACTCATCG GATGCCTTTC      3600

AATAAATTCG TCCAGGCATA AATCTTTTAA CCCAAATCAT TCATACCTCT CTCAACTAGA      3660

TGTAACTTAC AAAACCCCTG ACCTCATGAG CCACTTTCTT CCTCCTCATG AGGTCAGTTT      3720

TACTTTCTGC TGTTCCAGTA TCGTTTTTCC TCGCTAGATT TCCTCAAAAG GGCAGACTCC      3780

TCCCTTGGTT CGTCACACGA TTTTTTCATC TCGACTGTTC TTTAATGCAT CATTAACGAC      3840

GCTTTTCTTC TAGGTGGTTC ATAAGGAACA GGAAGATTCA GGTTGACTTT TCTAATCCTA      3900

GAATAAAGTG CTGAAAACAA TTCGGAATAG GCATAGAGAC TAGACAATTT GAGGAGCTGC      3960

TTGCGTCCTG TTCGAACACA TTTTCCCACC ACGTGAAGAA AAAGATGGCG                 4010
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(2) INFORMATION FOR SEQ ID NO: 254:

1279

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 2789 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```
ATGCATCCGT TTGTCAAGCC TAAATTGTAA TTTTTTTCAA TTTAAAACAG AAAAACCCAG        60

GAAAATGACA TAAAAATATC ATTCCTAGGC CTATTTATGC TATTTCTCTC TGAAAAATAT       120

GAGTATTCAG TCGGTCAAAT GAAGCTGAAC GAACTCATTT TCCCTCGCCT AATTCAATGA       180

TTCGATGACA TTGTTGGGCT ACATAAGCAT CGTGGGTCAC GATAATGACT GTTTTCCCCT       240

CTCGATTCAT CTCTAAGAGA AACTTCAAGA CCAAATCTCT ATTTTCAGGA TCCAGAGAAC       300

CTGTCGGTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTTAA GATGGCTCTA GCAACTGCAA       360

TTCGTTGTTG TTCGCCCCCA GACAACTCGG AGACCCTTTG ATGCAAAGTA GCTGATAAAC       420

CTACTCTCTC TAAAATCTCT TCCACCTTTT TGAGCTTGTC TTTCTTAGGC AATTTCACAT       480

ATTTCAGCGC CACATGAGAT TGTACTCGAC CGTTTCATCA TCAATCAGGG CAAAATTTTG       540

AAACAGATAA GAGATATGTT CACGGATTAT TGTTTGCGAC TTAGCAGAAT TAACCGCTAG       600

ATTTGTCTGA CCAAAAATCT CATACCGTCC GCTATAATCA CCATCTATCA AACCCAATAA       660

ATTTAACAAG GTCGACTTCC CACTACCACT CTTACCAACA ATAGCTACCA AATCCCCCTG       720

ATCAATCCTG AGAGATAAGT TATCCAAAAT CACTTTTCCC CCAATGGTTT TGGTAATATT       780

TTTCAACTCA ATCATAAGAT GCCCCCTTTC AATAACTCTA CTAGACTTCT TTTCTCCATC       840

CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG TAAAACCTGC AAACAGTAGA       900

AGTGGTAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA GAGGGAAACT ATAGCCCAGC       960

AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAGTT TCCACCCCAT AAACTTCTTG      1020

GTAATGATAT CCCTGCGCTT CAATAAGAAA GTTGTTACTA GTAAGAAGTA GGAAATCATC      1080

ATGCTAAGGA GACCAAACAA AGCAAAGAGT AGGTTAAAAT TCCGAACAGC ATCTCGATAA      1140

GAATCCACTT TCTCTTGTTG AATGGCTTGA ATAGATGAAA ATTTTAAATA ATTTCCATCT      1200

GACAATTTCT CAACTAACTC TGTAATCTCT TTTTGATGTT GAACCGTATT TTCAATTTTA      1260

ATCGGATTAT TTAAGCCAGT TGTTGACAGG GAGGCTTTCT CATCCCACAT CATATCAGAA      1320

TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCCT TTCGCTTATC ACTATATGGG      1380

AAAAATGACC AATCTCCTTC ATAATAGGCA ATCTCGACAT CCATCTCCTC TATCGTTCGT      1440
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                                         1280
TTTTGCTGCT CTTCATACTT CATCGAATGA AAGGCAATTA ACTTCCCCAA GAGCTGATTT   1500

TTATCTTCTT CACCTTTCGT ACTTGCTGGC ATCAAAATAA CTTTTTTAAT ACCGGTATTT   1560

GGTAGCTTGA ATCCCTTGCT CTTTAGAAAA TTGCGATTGG CATAGTAAAC ATCCACCGTA   1620

TCTGTTAACT GATATTGCTG AATCTGTTCT GATTGGACAA AATTTTTTAC AGGAAGACTG   1680

CTACTCTGCA CATAGCCCGC CTGCGTTTTT TCTACCAAAT CCTGATAAAA TCGATAGAAA   1740

TAATCTGTAG ATTTCCCTGA CCCTGCTAGC TCTTCTTGCC ACAGATTATC ATTGAGTTTG   1800

AAGGTTTCTA AGGTCAGGTA ATTACCTTGA CTTACCCACT GTTGCTGATA AGCAAGTTCT   1860

TTGTTTTCTT GTTCTAAACT TCTGCCCACC CCAATCAGTA AGGCCGTCAG TAAAATAGTT   1920

GTCCCTATTT TCATCACATA ATTGAAGATA AGACCAAATT TGAAAGATGA AAAACCTTTC   1980

AGCAGAGAGC TGATTGTCAT TTTTTGGATT AAGAGGTAAG TCAACCAACT GATAAAGAGA   2040

TAAAGCTGCA ACAGCAAAAA ATGAGACAAC CACAGCATAG GAAACAAATC TTTTGGCTTA   2100

TAATCAAGCA AGAAAAACAC GCCTAGATTG ATCACAAGAG CCCCACCTAG GAGGAGGTAA   2160

AGGTTGCCTT TTACAACATC AGCTAAAACA GCCCTATCTT GAAAACCAAG TAATTTTTGT   2220

ACCCCAACTC TTTTCATCTC CATCATCGGT TGATACACTG TCACTAACAC AAGAAGCAAA   2280

ATAGCCAAGA CAAAAACAAT GGCAGATAAA AGCAAATCTC GATTTATGAC TTCCACTGCA   2340

CTTTTGTAGG TCGGCTCTAG CAAGGTAGCC TGGTCTATCT TGAAAAAATC GCTCCATTTC   2400

TGTACAATCC TATCCTTGTC CATCTCTTGT GTAGAAGTTA TCGTATAGCG ACCATTTAAA   2460

CTACGAGATG TATCCTTGAT ATAGGTTTGA AAAGTCATAA GCTGAATAGG TTTGGCTTTT   2520

AGAAAGGTCG GAATCGTACC AAGTTTATTG GAAATTTCTT TATTACTATA GACTCCTTCA   2580

CCATCTGTGG TAAAATCAAG AGAAGAAATC CCAAACTCTT GGTAGGGGAA GGTATCTTTA   2640

TCAAAAACAC CAGACTTGAC CACCTCATCA CCACTGTCTG TTTTGATGAT GGAGACTTTA   2700

TACTCCTTTG ATACATCCTC AAAAAATCGA AGAACAGACG CTGCAGGTTC GTTAATATCT   2760

TTCAAATACA AATCCAAAGA ATCTACAGG   2789

(2) INFORMATION FOR SEQ ID NO: 255:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2495 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTGCGAATTT TATTAAAGAT AATGTGTTAA TTACAGCGGC TCACAACTAC TACAGACATG   60

1281

```
ACTATGGGAA AGAAGCGGAT GATATTTATG TTCTTCCGGC TGTTAGTCCA AGTCAAGAAC        120

CATTTGGAAA GATCAAAGTA AAGGAAGTTC GTTATTTGAA GGAATTTAGA AATTTAAATT        180

CTAAGGATGC AAGGGAATAT GACTTGGCTT TATTAATTCT AGAAGAGCCC ATTGGTGCAA        240

AATTAGGGAC TTTGGGTCTT CCTACTAGTC AAAAAAATTT GACAGGAATA ACTGTGACTA        300

TCACAGGCTA TCCATCATAT AATTTTAAAA TTCATCAAAT GTATACAGAT AAGAAACAAG        360

TTTTAAGTGA TGATGGCATG TTCTTGGATT ACCAAGTTGA TACTTTAGAG GGGTCTAGTG        420

GATCTACAGT TTATGATGCT AGTCACCGTG TAGTAGGAGT GCATACTTTA GGAGATGGAG        480

CTAATCAAAT TAACAGTGCA GTTAAATTAA ATGAACGAAA TTTGCCATTT ATTTAwTCGG        540

TTCTTAAAGG TTACTCTCTT GAAGGATGGA AGAAAATAAA TGGTAGTTGG TACCATTATA        600

GACAACATGA TAAACAAACG GGTTGGCAGG AGATAAATGA TACCTGGTAT TATTTAGACA        660

GTTCCGGTAA GATGCTTACA GATTGGCAAA AAGTCCATGG AAAATGGTAT TATCTCAATT        720

CAAATGGAGC AATGGTTACA GGTAGCCAAA CTATCGATGG TAAAGTTTAT AACTTCGCTT        780

CATCTGGTGA GTGGATTTAA TGTTGGAGGA TATATAAAAT GAAGCTTTTG AAAAAAATGA        840

TGCAAATCGC ACTAGCCACA TTTTTCTTCG GTTTGTTAGC GACAAATACA GTATTTGCAG        900

ATGATTCTGA AGGATGGCAG TTTGTCCAAG AAAATGGTAG AACCTACTAC AAAAAGGGGG        960

ATCTAAAAGA AACCTACTGG AGAGTGATAG ATGGGAAGTA CTATTATTTT GATCCTTTAT       1020

CCGGAGAGAT GGTTGTCGGC TGGCAATATA TACCTGCTCC ACACAAGGGG GTTACGATTG       1080

GTCCTTCTCC AAGAATAGAG ATTGCTCTTA GACCAGATTG GTTTTATTTT GGTCAAGATG       1140

GTGTATTACA AGAATTTGTT GGCAAGCAAG TTTTAGAAGC AAAAACTGCT ACGAATACCA       1200

ACAAACATCA TGGGGAAGAA TATGATAGCC AAGCAGAGAA ACGAGTCTAT TATTTTGAAG       1260

ATCAGCGTAG TTATCATACT TTAAAAACTG GTTGGATTTA TGAAGAGGGT CATTGGTATT       1320

ATTTACAGAA GGATGGTGGC TTTGATTCGC GCATCAACAG ATTGACGGTT GGAGAGCTAG       1380

CACGTGGTTG GGTTAAGGAT TACCCTCTTA CGTATGATGA AGAGAAGCTA AAAGCAGCTC       1440

CATGGTACTA TCTAAATCCA GCAACTGGCA TTATGCAAAC AGGTTGGCAA TATCTAGGTA       1500

ATAGATGGTA CTACCTCCAT TCGTCAGGAG CTATGGCAAC TGGCTGGTAT AAGGAAGGCT       1560

CAACTTGGTA CTATCTAGAT GCTGAAAATG GTGATATGAG AACTGGCTGG CAAAACCTTG       1620

GGAACAAATG GTACTATCTC CGTTCATCAG GAGCTATGGC AACTGGTTGG TATCAGGAAA       1680

GTTCGACTTG GTACTATCTA AATGCAAGTA ATGGAGATAT GAAAACAGGC TGGTTCCAAG       1740

TCAATGGTAA CTGGTACTAT GCCTATGATT CAGGTGCTTT AGCTGTTAAT ACCACAGTAG       1800
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1282

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GTGGTTACTA CTTAAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA ATTGTAAACT    1860

GTGATGGATA CTTAACTTTG TATAATAGGT GGATAAAAGT CTTCACAATC AAAAAACGCA    1920

TAGTATCAAG GTTTTTCTGT ACTGCCCTCA AACAGTTAGA CAATTAATTT ATCCGAAGgA    1980

TTTAGTTCTG TATTGCACAG GGCTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT    2040

GTAGTAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAAGCGACT GAAACGACTT    2100

CTCATAACCG TAAAACATTT CCGATTTCAG AATCCCAAAG AAGGACTCCA TCATACTATT    2160

GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG    2220

ATGATAAGAA TCGTGTTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA    2280

GTGCTTCTCT GTGAATGCCT GTTCCAACAT TGTTTGTACT TGTTCTAAGT TGGGTGAAGT    2340

TGAAAGATTA TAGGCGATAA TTTCGCTATT AAAGCCATCA AAAACTGGTG ATAAGTAAAG    2400

CTTTTGAGTA CTTGCTGGAA TGGCAAATTC TGTCACATCT GTGTAGCACT TTTCCATTGT    2460

TTTAGAGCCT TCAAATTGGC CTTGAATGAG ATTCG                               2495
```

(2) INFORMATION FOR SEQ ID NO: 256:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 870 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```
TACCACCGTA TTCATCCAGC AAGATTGCCA TTTGTCTTTG GGTATTTCGC AGTTCTTTTA     60

GCAAGTCATC CACAAAAATA GTTTCAGGTA CAAAAAGTGG ATCTTGTAAA ATTCTCTTCC    120

AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCTTAAG GAGACTCTTG GTGTGAATGA    180

TTCCAATTAC ATTGTCCTTA TCCCCATCAT AAACCGGGAT ACGAGAATAA TTTTGTTTTA    240

AAATACTTTG GATAATGGCT TGACTATCAT CCTGAATATC CACCATAAAG GCATCCGTTC    300

GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTAGCATCT    360

CAATCTCATC AGCATCCAAT GTTTCTTCAC TATTTGTCAG CATATAGGCA ATTTCATCAC    420

GGGTCATCTT TTCATCCGCA TCATCGAATG ACATAGGAGT CAAATGGCTC AAGAAATTGG    480

TCGAAGCAGC TAAAAGCCAA ACAAAAGGAC TGACTAGTTT TCCGATCCCA ATGATAATCG    540

GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAGAGC GATTCTCTTA GGATATAATT    600

CCCCAAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAGTT GCCACGGCTT    660

GTGCTGTTTC GCCATTCCCA AGCCAAGAGG CAATCACACG TCCTAGAGTA TCAGTTAAAC    720
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1283

TCGCCCCTGA TAAGATTGTA ATCAGGGTGA TTCCTACCTG GATGGTTGAT AAAAAGTGGT   780

TAGGATTTTC TAGTACCTTC AGCAGGCGGA TGTAGCGTCT GTCTCCTTCT TCCGCCTTTT   840

GTTCAACTCG GGCACGATTA AGAGAAACGG   870

(2) INFORMATION FOR SEQ ID NO: 257:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1245 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCCCAGA AGCCCGCATT CTCATCGCCA ATGTCGTGAT TGATTTGGCC CTTTCTCCAA   60

AATCCAACTC AGCCTATGTA GCTATGGATA AGGCACTTGC TGACCTCAAA ACATCAGGGC   120

ACTTGCCTAT TCCGCGACAC CTGCGTGATG GGCACTACAG TGGAAGCAAG GAACTGGGGA   180

ATGCCCAAGA CTATCTCTAT CCACACAACT ATCCTGGAAA TTGGGTCAAG CAAGACTATC   240

TGCCAGAAAA AATTCGTAAT CATCACTATT TCCAAGCAGA AGATACTGGT AAATATGAAC   300

GGGCTTTGGC TCAAAGAAAG GAAGCTATCG ACCGTTTGCG AAAAATCTGA AATCCTTTTC   360

AAAAAATTGC ACTTTCCTCT TGATTTTTTT TGAAAAAGTG GTATCATATA AATATAGAAA   420

CGCTGTGGTG TACGACTTCA CACTTAAGTG TTGACCGACT ATTTTTTGTA TTATTAGGGA   480

AACAAAAGTC TTCTAACAGC ATGTAGGCCG CTCTCACACGG AAACAGCTTC AGTTAGAGCG   540

AGTTGCCCAC CTGCTTAATT GCGCGGGTTC AATACAAACC GTGAAGTTTC GGCACCAATA   600

CAGCTTTTTT CTTTGCCTCC TTAGCTCAGC TGGCAGAGCA GCGGACTCTT AATCCGTGGG   660

TCACAGGTTC GATCCCTGTA GGGGGCATAT AAATACAACA GGAAAAGCCT TATAATATAG   720

GGCTTTTTTT GCTTTCCTTT TAAAAAATTGT CGTGCAATTT GCCGTGTTTT TACAACAAAC   780

TTTTCACAGC CATAAACTCC TCACTAATTT TTTCCTCCAA GGTATGCCCA TAAACGTCAA   840

TCAACATGGA GATATCTTTA TGTCCTAAAA TTTGGCTCTT TGTCAACTGT AGTGGGTTGA   900

AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCCTTTCT TTTTTGATAT TCAGAGCGAT   960

AAAAATCCGT TTTTTGAAGT TTTCAAAGTT CCGAAAACCA AAGGCATTGC GCTTGATAAG   1020

TTTGATGAGA TTATTGGTCG CTTCCAATTT GGCGTTAGAA TAGTGTAGTT GAAGGGCGTT   1080

GACGATTTTC TCTTTGTCCT TTAGAAAGGT TTTAAAGACA GTCTGAAAAA GAGGAGGAAC   1140

CTGCTTTAGA TTGTCCTCAA TGAGTCCGAA AAATTTCTCC GGTGCCTTAT TCTGAAAGTG   1200

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                                       1284
AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAC TCTTG                        1245
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(2) INFORMATION FOR SEQ ID NO: 258:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1684 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

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ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAAGAT AGTTTGTCTG        60

AAGCTGAGAG AGCGGCAcCC AGGCTTATGC TAAAGAGAAA GGTTTGACCC CTCCTTCGAC        120

AGACCATCAG GATTCAGGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCGCGT        180

GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC AATCTTCAAT ATACTGTAGA        240

AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAATTTGA        300

GTGGTTTGAC GAAGGCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC        360

GACTGTCAAG TACTATGTCG AACATCCAAA CGAACGTCCG CATTCAGATA ATGGTTTTGG        420

TAACGCTAGC GACCATGTTC AAAGAAACAA AAATGGTCAA GCTGATACCA ATCAAACGGA        480

AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAGAAACCC CTCGAGAAGA        540

GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAG AAGAATCACC        600

AGAGGAATCA GAAGAACCTC AGGTCGAGAC TGAAAAGGTT GAAGAAAAAC TGAGAGAGGC        660

TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT        720

CACAGGATTA AAAAATAATT TACTATTTGG CACCCAGGAC AACAATACTA TTATGGCAGA        780

AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTTCTAAC        840

TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAATG TGAGTTCTAG        900

TTCTCATTTT TTTCATGAAA ATGTGCAAAA TATAGTAGAT TGAAACTAGA ATAGTATACC        960

TCTACTTCTA AAACATTGTT AGAAATCGAT TTGACTGTCC TGTTCTTATT TCATTTTACT        1020

ATATCTTAAC AGATAGTGTA AATAAAGATA AACTATTTAC TGGCTAATTA ATCAGTTAAA        1080

CACTAGTTAA GGAGTAATGA TGAAAAAAAG AACAATACTA TTATTGATGG CCAGTCTGTT        1140

AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCTCATCA        1200

GGATTACTCT TTACTGCTAT TTTAGAAACT GGGGTGGTTT GATGGAAAGT ATTGGTCTTG        1260

TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAACTGATT AGTAAAGTAG        1320

CTAAAGATGT TCCGATTACT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT        1380
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<div align="center">1285</div>

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TTGAACAAGT AGATAGGGTT GTTTCCGAAA ATCCAGCAGA TACTTTACTT GCCTTTTTTG      1440

ACCTAGGTTC TGCTAAAATG AACTTAAAAA TGGTGACTGA TTTCAGTGAT AAAAGTATCA      1500

TCATCAACAG GGTTCCAATT GTAGAAGGTG CCTATAATGC AGCTGCTCTT CTTCAGGCTG      1560

GTGCAGAACT GTCAGTTATT CAAACACAGT TaGCGGAgCt TGAAATCAAT AAATAAGGAA      1620

TTTTACTATA ACTCTTTTTA TAGATAAGCT ATTGaTTATC TCAACTATAA TAATGTTAAG      1680

TnAA                                                                  1684
```

(2) INFORMATION FOR SEQ ID NO: 259:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 970 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```
AGGAGTGGAG AnATATGAAG ACACAAATTT TCACATTATT GAAAATCGTT GCTGAGATTA       60

TTATTATTTT GCCATTTCTA ACTAATCTAT AAGTTCTTTA TATTGCTGAA AACGCAATTC      120

AAAAAGGGCT ATTAATTGTG GATTTTCTAA TACCTGCAGA GATTGGATAA AGCGTTCAAT      180

CTCTTTTTGA TTGCTTCCCT TTGTTTGAAG AAAGACACTC ATCTTCTTTA AAAATTGCCA      240

CGATACTTTT TCAAAAACAT CATACGGTCG TAACATCCTC TCCAACTCGG CTTCGAAGAT      300

TGGGATGTAG GAGAAAAGTT TTCGCTCCAT GAGTTCTGAT AAGATATTTA AGAGTCCTTG      360

CTTCATATAC AATCGATTGT GTACTAACTC TTTAAATTCT TTGGATTTTT CGAGTAAGGA      420

GGTTGATAAA AAAATCAGAT CTTGATTGCT CAAGAAGGGC ATGGTATTGC AAAAGAGATA      480

GAGTTCAAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTCGCTATC      540

CTCCTCTGCT AGTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGGC      600

ATTCAAACGA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCCTCCA ATAGCTGCTC      660

TAAAGCAGCT ATATCCTGAT GGGCAAAGCG ATTCACAACC TTTCGACCGA TTCGCATATG      720

TGGAGATTCT TGATAGTTGT TGAGCTTGTG CCCAAACTCA TCAAAGGTCA CATTTATACC      780

TTGGATAGCT AGAATCAACT TATCCGCAGA CAGCATAGAC TGCCCTAGTT CAAACTTGGA      840

CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTCGCCAA      900

ACGTAATTCC TTGTAAAATT CCCCCAGTTC CATTCTCTCA ATCATCTGAC CACCTCCTAG      960

CTTTTGCAGG                                                            970
```

1286

(2) INFORMATION FOR SEQ ID NO: 260:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2996 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```
GTTGACCACG GGTAAAACTA CCCTAACTGC AGCTATCACA ACTGTTTTGG CACGTCGCTT      60

GCCTTCATCA GTTAACCAAC CTAAAGACTA TGCGTCTATC GATGCTGCTC CAGAAGAACG     120

CGAACGCGGT ATCACTATCA ACACTGCGCA CGTTGAGTAC GAAACTGAAA AACGTCACTA     180

CGCTCACATC GACGCTCCAG GACACGCGGA CTACGTTAAA AACATGATCA CTGGTGCTGC     240

TCAAATGGAC GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAAACTCG     300

TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA     360

AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT     420

ATTGTCAGAA TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA     480

AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA ACACAGTTGA     540

TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA     600

CGTATTCTCA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT     660

TAAAGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTCAAA AAGCAGTTGT     720

TACTGGTGTT GAAATGTTCC GTAAACAACT TGACGAAGGT CTTGCTGGAG ATAACGTAGG     780

TGTCCTTCTT CGTGGTGTTC AACGTGATGA AATCGAACGT GGACAAGTTA TCGCTAAACC     840

AGGTTCAATC AACCCACACA CTAAATTCAA.AGGTGAAGTC TACATCCTTA CTAAAGAAGA     900

AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC     960

TGACGTTACA GGTTCAATCG AACTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA    1020

CGTGACAATC GACGTTGAGT TGATTCACCC AATCGCCGTA GAACAAGGTA CTACATTCTC    1080

TATCCGTGAG GGTGGACGTA CTGTTGGTTC AGGTATGGTT ACAGAAATCG AAGCTTAATT    1140

CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAAGAATC TTGCTTGGCA    1200

AGGTTCTTTT TTTAGATATT GAACTAATAC TCAATGAAAA TCAAAGAGCA AACTATAATA    1260

TATTGAAACT AGAATAGTAC ACATCTACTT CTAAAACATT GTTAGAAATC GATTTGACTG    1320

TCCTGATCGA TTTGTCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC    1380

TCAAAACATT GTTTTTAGGT TGTAGATAGA ACTGACGAAG TCAGtAACAT CTATACGACA    1440
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1287

AGGCGAAGCT GACGCGGTTT GAAGAGATTT TCGAAGAGTA TAATACTAGA CTAAAATCAA   1500

AAAGCATTAT ACAATAGTAA TATGAAATCA ATTAAAGAAG AAATCCAAAC CATCAAAACA   1560

CTTTTAAAAG ACTCTCGTAC AGCTAAATAT CATAAACGCC TTCAAATCGT TCTATTTCGT   1620

CTGATGGGCA AATCTTATAA AGAGATTATA GAACTTTTAT AGTGGTTTGA AATAAGATGT   1680

GAACAACTCT ATCAGGAAAG TCAAACTAAT TTATAGAAAT ATTTTAGCAG CCAAGGTGTA   1740

CTGTTATAGA TTCAATACAC TTTAGACTGT AATCAAACAA CGATTTGGCG AAATGTAAAA   1800

AATATGAGGA GTTCGGACTC GACTCTCTCC TTCAAGAAAC ACGTGGTGGT CGTAACCATG   1860

CTTATATGAC GGTTGAGCAA GAGAAAGTCT TTCTTGCCCG CCATTTGAAG GCTACAGAGG   1920

CAGGAGAATT TGTTACAATT GATGCCTTAT TTCAGGCTTA TAAAAAGGAG TTAGGTCGTT   1980

CCTACACACG TGATGCCTTC TATCAACTGT TGAAGCGCCA TGGTTGGCGA AATATTACGC   2040

CACGTCCAGA ACATCCTAAG AAAGCAGATG CTCAAACCAT TGTCGCGTCT AAAAATAAAG   2100

TCTCAATTCA AGAAGACAAG TGAACTGCAC CCCAAAAGTT AGACAGAAAA AATCTAACTT   2160

TTGGGGTGTT TTTATTATGA AATTAACTTA TGATGATAAA GTTCAGATCT ATGAACTTAG   2220

AAAACAAGGA TATAGCTTAG AGAAGCTTTC AAATAAATTT GGGATAAACA ATTCTAATCT   2280

TAGGTACATG ATTAAATTGA TTGATCGTTA CGGAATAGAG TTCGTCAAAA AAGGAAAAAA   2340

TCGTTACTAT TCTCCTGATT TAAAACAAGA AATGATTCAT AAAGTCTGAC ATGAAGGCTG   2400

GACTAAAGAT AGAGTTTCTC TTGAATACTG TCTCCCAAGT CGTACGATAC TTCTTAACTG   2460

GCTAGCACAA TACAGGAAAA ACGGGTATAC TATTGTTGAG AAAACAAGAG GGAGAGTACC   2520

TGAGAGCGGA GAATGCCATC CTAAAAAAGT TAAGAGAACT CCGATTGAAG GAGGAAAAAG   2580

AGAAAGAAGA AAGACAGAAA TTATTCAAGA ATTAATGACT GAGTTTTCGT TAGATATTCT   2640

TCTAAAAGCC ATTAAACTAG CTCGTTTGAC CTACTACTAT CACTTGAAAC AGCTAGATAA   2700

ACCAGATAAG GACCAAGAGC TTAAAGCTGA AATTCAATCC ATTTTTATCG AACACAAGGG   2760

AAATTATGCT TATCGTCGGA TTTATTTAGA ACTAAGAAAT CGTGGTTATC TGGTAAATCA   2820

TAAAAGAGTT CAAGGCTTGA TAAAAGTACT CAATTTACAA GCTAAAATGC GACAGAAACG   2880

AAAATATTCT TCTCATAAAG GAGACGTTGG CAAGAAGGCA GAGAATCTCA TTCAAGGACA   2940

ATTTGAAGGC TCTAAAACAA TGGAAAAGTG CTACACAGAT GTGACAGAAT TTGCCG   2996

(2) INFORMATION FOR SEQ ID NO: 261:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 837 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

1288

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAAA TCAGAACAAG   60

GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAAAT AGTTGCAGTA GCATGATTTC   120

TCTCATTTCT ATCTTTTTTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTTCCTT   180

TATCTATTAT ATCAAATATA AGTCCGTTTG TAACTAGCGA AGAATTCTTT TGTCCGCTCT   240

TCTTTAGGGG TGTGGATAAT CTCATCCGGA GTTCCAGACT CGATGATTTT CCCCTTATCT   300

AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAAGGACA TGTCATGACT GACCAAAATC   360

ATGGTCTGAC CTGACTTAGC AGCATCTGCA ATAGACTTTT CTACTTCACC GACCAATTCT   420

GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAACAT CTGGTTTCAT AGCAAGCGCA   480

CGCGCTAGGG CAACCCGTTG CTTCTGTCCA CCTGATAAAT GGCGAGGATA ATGGTTTTCA   540

CGGTCCGAAA GCCCAACCTT AGCCAACTCT TCCTTGGCAA TCTTAGTCGC TTCTTGGTCA   600

GATAATTTCT TGCAACAAC CAAGCCTTCT TTCACATTAT CAAGTGCTGT TCGGCGTTCA   660

AACAAATTAA ACTGTTGGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTTCTTCT   720

TGAGTGATTT TAGAAAAATC AACTGAAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT   780

GTTTCTAGAT AATTGAGACT GCGAGAAAGG TTGATTTTCA GCTCTGAAGA CCAATCA   837

(2) INFORMATION FOR SEQ ID NO: 262:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 868 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAAA TGGGCTAATT AGATTATAGT AAGAAAGGTA AGTTAAAAAT GAGAATTGCA   60

ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGGCGG TTTCAGAATT TTTGAAATCA   120

AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAATC   180

TTTGGTAAAA AAGTAGGGGA AGCTGTAACT AGCGGTCAAG CTGATCTTGG AGTATGTATC   240

TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCTGCC   300

TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAAGAAC AATTGAACGC TAACGTTATT   360

GGTTTTGGTG GTAAAATTAC TGGTGAATTG CTTATGTGTG ATATCATCGA AGCTTTCATC   420

1289

CATGCTGAAT	ACAAACCAAC	TGAAGAAAAC	AAAAAATTGA	TTGCGAAAAT	TGAACATGTT	480
GAAAGTCACA	ATGCTCAACA	AACAGACGCA	AACTTCTTTA	CAGAATTCCT	TGAGAAATGG	540
GATCGTGGAG	AATACCACGA	CTAAGAGGTG	ACCTATGATT	TTAACAGTCA	CAATGAACCC	600
ATCCATCGAT	ATTTCCTATC	CCTTGGATGA	GTTGAAGATT	GATACTGTCA	ATCGTGTGGT	660
GGATGTAACC	AAAACGGCTG	GTGGTAAGGG	ACTCAATGTT	ACCCGAGTAC	TTTCAGAATT	720
TGGCGATTCT	GTTCTTGCTA	CTGGTTTAGT	GGGTGGCAAA	CTTGGTGAGT	TTTTGGTTGA	780
ACATATCGAT	AATCAAGTAA	AGAAAGATTT	CTTCTCAATT	AAGGGAGAAA	CTCGTAACTG	840
TATCGCTATT	CTCCACGGAG	ACAACCAA				868

(2) INFORMATION FOR SEQ ID NO: 263:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3744 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGTTCAAAG	TCTTCATAAG	ACTCGAAAGT	CACAGTTCTT	TCGTTCTTGC	TGGCATCTAT	60
ATAGGTAATT	TCAATCATGT	TTAAAACTCC	TTTGTTTAAT	GCTAACTTTA	TTTTACTCCT	120
TATAAAAGAG	AATGTCAAGA	AAAATGATTG	CGCACGCAAC	TTTTTTTAAA	ATCATCTTAA	180
ATCAAGAAAT	CCAAACCTGC	TTCCAAGCTT	TCTTCGACAG	TCTTTTGTAG	CGAGGCCAGT	240
GTCTTTTGCC	CATCATTTGT	CAGGCAGATA	AAACTAGAGC	GTCTATCTTG	ATGGCAACAC	300
ATGCGACTGA	GTAGACCGCA	ATTTTTAGCT	TCCAAGCGAG	CCACCATCCT	AGAAACTGCG	360
CTCGGGCTCA	GATGAAGCTT	ATCTGGCAGG	TCAATCTGGC	GTAGAGATTT	TTCTTCAGCC	420
AAGTCCAGAT	AGTAGAGCAG	GTAGAACTCT	TTCAAGGTCA	GACTTTGCTC	GCTCTGTTGG	480
GCAATGGTCT	CTTCCAAGAG	ACTTTCAATT	TCTTTCTGAC	GCCGATTGAA	GTCAAACCAT	540
TTTTCCAAAT	AGGTCATAGT	GTCTCCTTTC	TTTTTAGAGT	CATAAATAGA	AGAAAGTCCA	600
TTAACGGGCA	GTCTCTGCGT	CACAAGATGA	TTGCGCATGC	AATAATTATA	CTACTTTTCA	660
AGAATGCTGG	CAAGCTCTGT	TTTTTAGTGG	TTTTATTTTT	GTGTGAATAA	TGGGGGAATC	720
CTATTGTTTC	AATTTCTAAC	TCCTTATCAC	ATTCGAATTC	AGATTTTATT	TCATTTCTCT	780
ATCTATAGTT	GCTTAGTTTA	AAATAAGCAT	GGTCTAATAA	AGCTATGCAT	ATAGTACTGA	840
TTTTAAACAA	GGAGCATTAG	ATTCCATTAA	AGGAGGGCAC	AGACATGTCG	AGGCGGCCAA	900

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                                    1290
AGTTTTTGAT GTCGGCGTCA GAACTCTCTT CACGTGGGAA AAGAAAGACG TAAACAAGGG    960

AACTTAGAGC GGAAAAAGCG AGTCGTCAAA AAGCGTAAGA TCCCTTTAGA AGAATTGAAA   1020

GCCTTTGTAG AGGCTCATCC AGACGCTTTT TTACGGGAAA TTGCGGCCCG TTTTGATTGT   1080

GCTTTGCCCT CCGTATGGGC AGTTTTAAAG CAGATTAAGG TCATTTTAAA AAAGACGACC   1140

AGTTTTAGGG AACAAAAGCC TGAGAAAGTT TCTGAGTTTC TTGATATTTT GGATAACCTA   1200

AAAGATTTAC CAGTCCTATA TATTGACGAA ACGGGAATCG ACCGCTACCT CTATCGTCCT   1260

TATGCAGGGG CTCCTAGAGG GGAGAAAGTC TATGGCAAGA TTAGCGGACG GCGTTTTGAG   1320

CGGACTAATG AGGTGGAGCA AAAACTCAAT GGTAGTTTTC TAATCAGATA TATTGATTCA   1380

CAAATTAGAG AATGAAAGAA TAATTATGCA TAAAAATAGG AATATAAACC AAAAATTAGC   1440

TGATTTATAC TCATTTGCGT GTCTTTATAA AAAACTTATC TTATAATATA TATATATATA   1500

TATACAAAAT AGTAAAATGC TTTTTTTTTT TAGCAAAAAT ACCTCAAGTT TCTTGCTATT   1560

TTGGGTTCCC TATTCTATAA TTATAGTATG GTAATTTATT TATATCCATA CATGAAAATA   1620

ATACTCGAAA GGAAATTTCA AAATATTTTT TAGACGTCAG AAGGGTGAAT ATAGAGAAAC   1680

AGACCGAGTA ACTCGGTTCA AATTAATCAA ATCAGGGAAG CATTGGCTAC GGGCCTCGAC   1740

TTCTCTTTTT GGCTTGTTTA AGGTCTTGCG AGGTGGTGTT GATACTACTC AGGTCATGAC   1800

CGAAACGGTA GAAGATAAAG TAAGTCATTC AATTACTGGG CTTGATATCC TCAAGGGGAT   1860

AGTTGCTGCG GGAGCTGTCA TAAGTGGAAC CGTTGCAACT CAAACGAAGG TATTTACAAA   1920

TGAGTCAGCA GTACTTGAAA AAACTGTAGA GAAAACGGAT GCTTTGGCAA CAAATGATAC   1980

AGTAGTTCTA GGTACGATAT CTACAAGTAA TTCAGCGAGT TCAACTAGTT TGTCAGCTTC   2040

AGAGTCGGCA AGTACATCTG CATCTGAGTC AGCCTCAACC AGCGCTTCGA CCTCAGCAAG   2100

TACAAGTGCA TCAGAATCAG CAAGTACATC GGCTTCGACA AGTATTTCTG CATCATCTAC   2160

TGTGGTAGGT TCACAAACAG CTGCCGCTAC AGAAGCAACT GCTAAGAAGG TCGAAGAAGA   2220

TCGTAAGAAA CCAGCTAGTG ATTATGTAGC ATCAGTTACA AATGTCAATC TCCAATCTTA   2280

TGCTAAGCGA CGCAAGCGTT CAGTGGATTC CATCGAGCAA TTGCTGGCTT CTATAAAAAA   2340

TGCTGCTGTT TTTTCTGGCA ATACGATTGT AAATGGCGCC CCTGCAATTA ATGCAAGTCT   2400

AAACATTGCT AAAAGTGAGA CAAAAGTTTA TACAGGTGAA GGTGTAGATT CGGTATATCG   2460

TGTTCCAATT TACTATAAAT TGAAAGTGAC AAATGATGGT TCAAAATTGA CCTTTACCTA   2520

TACGGTTACG TATGTGAATC CTAAAACAAA TGATCTTGGT AATATATCAA GTATGCGTCC   2580

TGGATATTCT ATCTATAATT CAGGTACTTC AACACAAACA ATGTTAACCC TTGGCAGTGA   2640

TCTTGGTAAA CCTTCAGGTG TAAAGAACTA CATTACTGAC AAAAATGGTA GACAGGTTCT   2700
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1291

ATCCTATAAT	ACATCTACAA	TGACGACGCA	GGGTAGTGGG	TATACTTGGG	GAAATGGTGC	2760
CCAAATGAAT	GGTTTCTTTG	CTAAGAAAGG	ATATGGATTA	ACATCATCTT	GGACTGTACC	2820
AATTACTGGA	ACGGATACAT	CCTTTACATT	TACCCCTTAC	GCTGCTAGAA	CAGATAGAAT	2880
TGGAATTAAC	TACTTCAATG	GTGGAGGAAA	GGTAGTTGAA	TCTAGCACGA	CCAGTCAGTC	2940
ACTTTCACAG	TCTAAGTCAC	TCTCAGTAAG	TGCTAGTCAA	AGCGCCTCAG	CTTCAGCATC	3000
AACAAGTGCG	TCGGCTTCAG	CATCAACCAG	TGCCTCGGCT	TCAGCGTCAA	CCAGTGCGTC	3060
AGCTTCAGCA	AGTACCAGTG	CTTCAGTCTC	AGCATCAACA	AGTGCTTCAG	CCTCAGCATC	3120
GACAAGTGCC	TCGGCTTCAG	CAAGCACATC	AGCATCTGAA	TCAGCGTCAA	CCAGTGCTTC	3180
GGCTTCAGCA	AGTACCAGTG	CTTCAGCTTC	AGCATCAACC	AGCGCCTCGG	CCTCAGCAAG	3240
CACCTCAGCT	TCTGAATCGG	CCTCAACCAG	CGCCTCGGCC	TCAGCAAGCA	CCTCAGCTTC	3300
TGAATCGGCC	TCAACCAGCG	CCTCAGCCTC	AGCATCAACG	AGTGCTTCGG	CTTCAGCAAG	3360
CACAAGCGCC	TCGGGTTCAG	CATCAACGAG	TACGTCAGCT	TCAGCGTCAA	CCAGTGCTTC	3420
AGCCTCAGCA	TCAACAAGTG	CGTCAGCTCA	GCAAGTATCT	CAGCGTCTGA	ATCGGCATCA	3480
ACGAGTGCGT	CTGAGTCAGC	ATCAACGAGT	ACGTCAGCCT	CAGCAAGCAC	CTCAGCTTCT	3540
GAATCGGCCT	CAACCAGTGC	GTCACCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	3600
CCAGTGCTTC	AGCCTCAGCG	TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	3660
CATCAACCAG	TGCGTCAGCC	TCAGCAAGTA	CTAGTGCATC	GGCTTCAGCA	TCAACCAGTG	3720
CCTCGGCTTC	AGCGTCAAAC	AGTG				3744

(2) INFORMATION FOR SEQ ID NO: 264:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 795 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAAGAG	GCCTTGAGTA	ATCTCAATTT	GCAGATTGAA	AATGGAGAGA	TTATGGGCTT	60
GATTGGTCAT	AATGGGGCTG	GAAAATCGAC	CACTATAAAA	TCCCTAGTCA	GTATCATTTC	120
ACCCAGCAGT	GGTCGTATTT	TGGTAGACGG	TCAGGAGTTA	TCGGAAAATC	GCTTGGCTAT	180
TAAACGAAAG	ATTGGCTACG	TAGCAGACTC	GCCTGACTTA	TTTTTACGCT	TAACGGCCAA	240
TGAATTTTGG	GAATTGATCG	CCTCATCCTA	TGATCTGAGT	AGATCTGACT	GGAGGCTAG	300

1292

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TCTAGCTAGG CTATTGAACG TTTTTGATTT TGCTGAAAAT CGCTATCAGG TTATTGAAAC      360

TCTTTCTCAC GGAATGCGTC AGAAAGTCTT TGTCATCGGA GCACTCTTGT CTGATCCCGA      420

TATTTGGGTC TTGGATGAAC CCTTGACTGG TTTGGATCCC CAGGCTGCCT TTGATTTGAA      480

ACAGATGATG AAGGAACATG CACAAAAAGG GAAGACAGTC TTGTTTTCAA CTCATGTCCT      540

AGAGGTGGCA GAGCAAGTCT GTGATCGGAT TGCCATTTTG AAAAAGGGGC ATTTGATTTA      600

TTGTGGTAGT GTAGAGGACT TGAGAAAAGA TTACCCAGAC CAGTCTTTGG AAAGTATCTA      660

CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT TGCGGATGCG TCTCAAGGTC ATTAAAAAAT      720

TAGTTGATAT CAATATCCTT TATTCATCTC AAGAAGCTAA TCTGGCTAAT CTACGAAAGA      780

AGCAGGCTAA GAATC                                                      795
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(2) INFORMATION FOR SEQ ID NO: 265:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2231 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

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TGGTAATGTG CTTGGCAGCw TCCTTGACAC TGCTACTACC ATTTCCCATA GCGACCGACA       60

TACCAACGCC AGCCAGCATT TCAAGATCAT TATCTGAGTC ACCAAAAGCC ATGACTTGGT      120

TGAGGTCAAA GCCATATTCT TTCCCAACTC GGCGAATGCC TTCTAATTTA GAATTTCCCT      180

GATTGATGAC ATCCGATGCA AAAGGATTGC TACGTGTCAA TTTCAAGTCT TCAAAATCAG      240

CTGCCGCCTT CTCAGATTCT TCTGGTGTCA TCAGCATCAA AACTTGGTAG ATAGGCTGAT      300

TCATCAGGTG AAGCAGGTCC TCTTCCTTTT GGGGAACAAC CTTGCTGACC ATGCGATTAA      360

AAGACTGACT CACCGTCCGA GTTAAAACAG AGGGAACGAA GCGACTAATT CGTTGGGAAA      420

AAGAACCCAG ACCAAAGGAC ATGATTTTAG AACCCAACAT GGCATCCTTG GTCCCTAGAG      480

CAATCTCCGT GCCCTCTTTT TTAGCATAGC TAATTAGATG GCGCAAATGT AACTTGGAAA      540

TAGGGCTCGT GAACAAGACT CTGTCTTTAC TAAAGATATA CTGGCCATTA TAGGTTACCG      600

CAAAATCCAG ATCCAAATCG TCCATCAATT CCTTAACAAA AAAAGGTCCT CGCCCTGTCG      660

CTACGCCAAC TAGTACCCCT TGTTCTTTGA CAATCTTAAT CGCATCCTTA GTGGATTTCA      720

AAACACTCTT GCGATTGTTG ACCAAGGTTC CATCGATATC AAAAAAAACA GCTTTGACTT      780

CCATCCTATC CCAATCTCCC CTTTTGTGAT ACAATGATTA TACCACATTT CAGAAAGAGT      840

GAGTAAATCA TGCCTAAGAA AATCCTTGTT TTACATACGG GTGGAACTAT TTCCATGCAG      900
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1293

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GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC    960

CCACTTGAAG GAATCCAAGT CCACGCCTTG GACTTTTTTA ACCTTCCAAG TCCCCATATC   1020

AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAAG AGGAAGCAGA TAACTACGAT   1080

GGAGTGGTGA TCACACACGG AACCGATACT TTAGAGGAAA CAGCCTATTT CCTTGATACC   1140

ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TGCGTACtCC AATGAGCTCG   1200

GTAGTGATGG TGTTTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGGCTG   1260

CTGACAAAGG AGTTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA   1320

AAACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTTGGTCTCA   1380

TCATGAAACA GGAAATCCTC TACTTCAAAA CAGCTGAACC TCGTGTTCGC TTTGACCTTG   1440

ATCACATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA   1500

TTGATATGCT GGATTTAGAA CACTTGGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA   1560

ATATTCCCAA AGAAACGGCT CAAAAATTAG AAAGCCTTCT GCAAAAAGGA ATTCCAGTCG   1620

CTCTGGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAGGGTGGGG   1680

GCGTACAGTT GCAAAAAGCA GGCGTTTTCT TTGTTAAAGA ACTCAACGCC CAAAAAGCTC   1740

GCTTGAAACT CCTCATCGCC CTCAATGCCG GACTAACAGG ACAGGCTTTG AAAGACTATA   1800

TGGAAGGCTA ATACTCTTCG AAAATCTCTG CAAACCACGT CACGTCGCCT TACCGTATGT   1860

ATGGtACTGA CTTCGTCAGT TTCATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG   1920

TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGT TCTATCTACA   1980

ACCTCAAAAA CATGTTTTGA GCTGACTTCG TCAGTTCTAT CTACAACCTC AAAAACATGT   2040

TTTGAGCTGA CTTCGTCAGT TCTATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG   2100

TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGk TCTATCTACA   2160

ACCTCAAAAA CATGTTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAAACATGT   2220

TTTGAGCTGA C                                                        2231
```

(2) INFORMATION FOR SEQ ID NO: 266:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1310 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

1294

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GAGTCAAAGG CTCCGAGGTT GACTTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG      60

TCAGAAATTC TCTTCTTTGA AACAGAAGGG AGCAAGATCT ACGCTCATAA CCAGAAGGAA     120

GCTTATGAGG TTCGCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCCTCG CTATTTTAAT     180

CGAGTTTCCA AGTCAACGAT CGCAAACATC CGTCAGATTT ACTCAGTGGA CAAGTCCTTT     240

TCAGGAACGG GCACCATTTC CTTTTATCAG ACGCACAAGG AGGTTCATGT CTCACGGCAT     300

TACCAATCCC TCCTAAAGA AAAATCTAAGA AACATGAGGT AAAAAACATG AAAAAGAAAG     360

CATTTGGTAT TGTTTTATTG GTTTTAGCAG CTTGGATCTT GCTGCAAGGG AATTTTGGAA     420

TTCCTTCTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT     480

CCATTGAGTC CATCCTTAGA CGTCATCTCA CTTCGGCAGT TTTTACAGGT TTACTGGCGC     540

TCATCATTGC AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATTCT CTTATTTGGG     600

CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAAGTAAG TTCTGGAATG     660

AAAAAAAATG GTGGTACAAT GGGAAAAAAA CAGTCGTCAC GGATAAGGAA GTCGCTTTTG     720

GTAGCGGGAC CTTCTATAAG CAAGATCAAG ATCTCGTAGA TGACCAAGTG GAAGTCGCTT     780

TTGGGGATGC TAAAATCTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA     840

ATATTGAAGT GGCCTTCGGG AATGCAACCG TCTATGTTCC ACAACACTGG CGTGTAGATT     900

TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCCTGTAGCC CCAACCAGCA     960

AAACCTTGAT TATCCGTGGA GATGTGGCTT TTGGGAAGTT GGAAATTGTC TACGTTAAAT    1020

AAAAAAAATCT TCACTTCAAC CATCAAAATA GACGTACTAA GAGTAGGAAA TTGATGCCTT    1080

GCTCTGATTT CAGTTCTATG GTTGTTAGAC TTTAAAAAAT GAAATGCTGC CTTTAAAAGT    1140

TGTATATTTT TCGATATTTT GGCTTTTACG TTTGATGTAT CTATGTACTA CAGCGTAGAT    1200

GATGTAGTGT CAAATGCTTT TAAAAAACGG ATGATATTGG ACAGTTTTTT TGCCTTTAAT    1260

TGCTCAGGAA CCATGAAAGT CAGTACCTGG GTTTATGACA AGGGAGAATG              1310
```

(2) INFORMATION FOR SEQ ID NO: 267:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5922 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```
ACTCTGATTT GATTGGAACG ACAGTCGGTG CCATTGCAGT TACTTCAAAC GTAACGACTT      60

ATGTTGAGTC TGCTGCTGGT ATCGGTGCAG GTGGACGTAC TGGTTTGACA GCCTTGGTTG     120
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1295

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TAGCTATCTG TTTTGCGATT TCAAGCTTCT TTAGCCCACT TCTAGCGATC GTACCAACAG      180

CGGCTACAGC TCCAATCTTG ATTATCGTTG GGATTATGAT GCTTGGTAGC TTGAAAAATA      240

TCCATTGGGA TGATATGTCT GAAGCAGTTC CTGCCTTCTT CACATCTATC TTTATGGGAT      300

TCAGCTACTC TATCACTCAA GGGATTGCAG TTGGTTTCTT GACTTACACT TTGACTAAGC      360

TTGTTAAAGG TCAAGTTAAA GATGTTCATG TCATGATTTG GATTTTGGAT GCCTTGTTTA      420

TCCTTAACTA CATCAGCATG GCCTTATAAT AGAATGACCC AGGGGGATTT CCCCCCTTTT      480

TTAATACAaG GAGATAGGTG ATGAAAGAGA AAAATATGTG GAAAGAATTG TTGAATCGTG      540

CAGGCTGGAT TTTGGTCTTT TTACTTGCCG TCCTTTTATA TCAGGTTCCC CTAGTGGTTA      600

CCTCTATTTT GACTTTAAAA GAAGTAGCCC TGCTACAGTC AGGGCTGATA GTTGCTGGCC      660

TTTCAATTGT GGTTCTGGCT CTATTTATTA TGGGAGCTCG TAAAACCAAG TTAGCTAGTT      720

TTAATTTTTC TTTTTTTAGA GCTAAAGATT TGGCACGTTT GGGCTTGAGT TATCTAGTTA      780

TTGTCGGGTC AAATATACTT GGTTCCATTT TATTGCAACT GTCAAATGAG ACGACAACAG      840

CTAACCAGTC TCAGATTAAT GATATGGTTC AAAATAGTTC GTTGATTTCC AGTTTCTTCT      900

TGCTAGCCTT GCTTGCTCCG ATTTGTGAGG AAATCTTGTG TCGTGGGATT GTTCCTAAAA      960

AGATTTTCCG AGGCAAGGAG AACTTGGGAT TTGTAGTCGG TACGATTGTG TTTGCTTTAT     1020

TGCATCAACC AAGTAATTTA CCTTCTTTAT TGATTTATGG AGGTATGTCG ACAGTTCTAT     1080

CTTGGACAGC CTACAAGACC CAACGTTTGG AAATGTCGAT CTTGCTTCAC ATGATTGTTA     1140

ATGGGATTGC TTTCTGTTTG TTGGCTCTTG TGGTGATTAT GAGTCGGACA TTAGGAATTT     1200

CTGTTTAAAA GTTTTTATGT AGGAACCGAC CTCTTTCTAC CAGGGAAAGA TGAATGCAAT     1260

CGTGTCCATC TTTTTCTTTT TATGGTAAAA TAGAAAAATA ATATGATGAA AATCCTTGAG     1320

GGAGTGACCG ATATGTCAAG TAAAGCCAAT CATGCAAAGA CAGTTATTTG CGGAATTATC     1380

AATGTAACCC CAGACTCCTT TTCGGACGGT GGTCAATTTT TTGCTCTTGA GCAGGCGCTC     1440

CAGCAGGCTC GTAAATTGAT AGCAGAAGGA GCCAGTATGC TAGATATCGG CGGAGAATCG     1500

ACTCGGCCGG GAAGTAGCTA TGTTGAGATA GAAGAGGAAA TCCAGCGTGT TGTTCCAGTG     1560

ATCAAAGCGA TTCGCAAGGA AAGTGATGTC CTCATCTCTA TTGATACTTG GAAGAGTCAA     1620

GTAGCAGAGG CTGCTTTGGC TGCTGGTGCC GATCTAGTCA ATGATATCAC TGGTCTTATG     1680

GGTGATGAGA AAATGGCTTA TGTGGTAGCT GAAGCGAGAg CGAAAGTGGT CATCATGTTT     1740

AACCCAGTTA TGGCTCGACC TCAGCATCCT AGTTCGCTTA TCTTCCCTCA TTTTGGTTTT     1800

GGTCAAACCT TTACAGAAAA AGAGTTAGCT GACTTTGAAA CATTGCCAAT CGAAGACTTG     1860
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                                   1296
ATGGTGGCTT TCTTTGAACG AGCACTAGCG AGAGCGGCAG AAGCTGGTAT TGCACCAGAA        1920

AATATCCTGT TGGATCCAGG AATTGGCTTT GGTCTGACCA AGAAAGAAAA TCTGCTTCTT        1980

TTACGGGACC TGGATAAACT ACATCAGAAG GGCTATCCAA TCTTTCTCGG AGTGTCGCGC        2040

AAGCgATTTG TCATCAATAT CCTAGAGGAG AATGGTTTTG AAGTCAATCC TGAGACAGAG        2100

CTTGGTTTCC GAAATCGGGA CACGGCTTCG GCTCATGTAA CTAGTATCGC TGCGAGACAG        2160

GGTGTAGAAG TGGTGCGCGT GCATGACGTA GCTAGTCACA GGATGGCAGT TGAAATTGCC        2220

TCTGCCATTC GTCTGGCTGA TGAAGCGGAA AATTTAGATT TAAAACAATA TAAATAAGAT        2280

GAAAGAAATT GAAAACAATC AGTGGATTGC TAACTACCGG ACGGATCAAC CGCATTTTGG        2340

CTTGGAACGA ATGGTGGAAC TGTTAGCTTT GCGTGGCAAT CCCCATCTCA AACTCAAGGT        2400

CCTCCATATC GGAGGGACTA ACGGCAAGGG CTCGACTATT GCTTTTTTGA AAAAGATGCT        2460

AGAAAAGCTA GGGTTGAGAG TTGGCGTGTT TAGCTCGCCC TATCTCATTC ATTACACAGA        2520

CCAGATTAGC ATCAATGGGG AATCGATCTC AGAAGCGAGG CTAGAAGCTC TCATGGCAGA        2580

CTATCAGTCT TTGCTGGAGG GAGAAGCGGT CGCCAATTTA CAGGGCACAA CCGAGTTTGA        2640

GATTATCACA GCCCTGGCCT ATGACTACTT TGCCTCAGAG CAAGTAGATG TGGCCATCAT        2700

GGAAGTTGGC ATGGGTGGAC TTTTGGATAG TACCAATGTC TGTCAGCCCA TTTTGACAGG        2760

AATTACAACT ATTGGCTTGG ATCATGTGGC TCTACTTGGT GACACCTTGG AGGTCATAGC        2820

AGAGCAGAAG GCAGGTATTA TCAAACAAGG GATGCCCTTG GTAACAGGGC GTATTGCTCC        2880

AGAAGCCTTG GCTGTGATTG ACCGCATTGC GGAAGGGAAA GATGCGCCGA GACTTGCCTA        2940

CGGGACAGAT TATCAGGTTC GTCATCAAGA AAGTGTGGTG ACAGGGGAAG TCTTTGACTA        3000

TACAAGTGCT GTCAGACAAG GTCGCTTCCA GACTAGCCTG CTTGGTTTGT ACCAAATAGA        3060

GAATGCTGGG ATGGCCATAG CTTTACTTGA TACTTTTTGT CAAGAAGATG GTCGAGAGCT        3120

AGCAAGCAAT GATTTTCTTG GTCAAGCCTT GGAAGAAACA AGTTGGCCAG GGCGTTTGGA        3180

AATCGTGTCA AGAGATCCCT TGATGATTTT GGATGGAGCC CACAATCCCC ATGCTATCAA        3240

GGCCTTGTTG GTAACCTTGC AAGAACGTTT TGCGGATTAT CATAAGGAAA TCCTCTTCAC        3300

TTGTATCAAA ACCAAGGCCT TGGAGGATAT GTTGGACTTG CTGGGAGCCA TGCCAGTTAC        3360

CGAGCTTACT CTAACACATT TTGCGGATAG TCGGGCGACG GATGAAAACG TGCTGAAAGA        3420

GGCAGCTAAG TCTAGAAATC TCAGCTACCA AGATTGGCAT GATTTTCTAG AGCAGAATTT        3480

GACAGATAAA AAAGAAGAGA AACAAACAGT TAGGATTGTC ACAGGTTCCT TGTATTTCTT        3540

GAGCCAAGTG AGGGCCTATC TGATGGAGAG GAAGAACGAG AATGGATACA CAAAAGATTG        3600

AAGCGGCTGT AAAAATGATT ATCGAGGCTG TAGGAGAGGA CGCTAATCGC GAGGGCTTGC        3660
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1297

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AGGAAACACC TGCTCGTGTA GCCCGTATGT ATCAAGAGAT TTTTTCAGGT CTTGGTCAAA    3720

CAGCAGAGGA ACATTTGTCA AAATCCTTTG AAATTATTGA CGATAATATG GTGGTAGAAA    3780

AGGATATCTT TTTCCATACC ATGTGTGAAC ACCACTTCTT GCCATTTTAT GGTAGAGCGC    3840

ACATTGCCTA CATTCCAGAT GGTCGTGTGG CAGGCTTGTC TAAGCTAGCC CGTACGGTTG    3900

AAGTTTATTC GAAAAAACCA CAAATTCAAG AACGTTTGAA TATCGAAGTG GCCGATGCCT    3960

TGATGGACTA TCTAGGTGCT AAAGGAGCCT TTGTTGTCAT TGAGGCGGAA CATATGTGTA    4020

TGAGTATGCG TGGTGTTAGA AAACCAGGCA CTGCAACCTT GACGACAGTA GCTCGTGGTC    4080

TATTTGAAAC AGATAAGGAT CTCCGTGACC AAGCTTATCG TTTAATGGGG CTATAAAAAG    4140

AATCCGCTTC AAGCGGATTT TTCTAGAAAG GAATCATTAT GGATCAACTG CAGATTAAGG    4200

ATTTGGAAAT GTTTGCCTAT CATGGTCTTT TTCCTAGTGA GAAAGAATTG GGGCAGAAAT    4260

TTGTCGTTTC AGCCATCCTA TCCTATGATA TGACCAAGGC AGCTACAGAC TTGGATTTAA    4320

CAGCCTCTGT CCATTACGGA GAATTGTGTC AGCAGTGGAC GACTTGGTTT CAGGAAACGA    4380

GTGAAGATTT GATTGAAACG GTAGCCTATA AACTGGTGGA ACGTACCTTT GAGTTTTATC    4440

CTCTTGTCCA AGAAATGAAG TTGGAACTGA AAAAACCTTG GGCACCGGTG CATTTGTCAC    4500

TAGATACTTG CTCGGTAACC ATTCATCGCC GCAAGCAACG AGCCTTTATC GCCCTAGGAA    4560

GCAATATGGG AGATAAACAA GCAAACTTGA AGCAAGCCAT TGACAAACTG CGAGCTCGTG    4620

GCATCCATAT TCTCAAAGAG TCCAGTGTCT TAGCGACGGA GCCTTGGGGT GGAGTGGAGC    4680

AGGATAGCTT TGCCAATCAA GTGGTTGAGG TGGAAACCTG GCTACCAGCA CAAGACTTGT    4740

TAGAAACCTT GTTAGCCATT GAGTCAGAGC TGGGACGGGT GAGAGAAGTG CATTGGGGAC    4800

CTCGTTTGAT TGATTGGGAC TTGCTCTTTG TGGAGGACCA GATCCTTTAT ACAGACGACC    4860

TCATATTGCC TCATCCTTAC ATAGCGGAAC GCCTTTTTGT CCTTGAGTCt TACAGGAAAT    4920

TGCGCCTCAT TTTATCCATC CGATATTAAA ACAACCGATC CGCAACTTGT ATGATGCTTT    4980

GAAAAAATAG AAAAACTCTA GTTTTCAGTT ACTTGCAACT GAAGGCTAGA GTTTTTATAC    5040

TCTTCGAAAA TCTCTTCAAA CCACGTCAGC GTCGCCTTAC CGTACTCAAG TACAGCTTGC    5100

GGCTAGCTTC CTAGTTTGCT CTTTGATTTT CATTGAGTAT TAAAATAGGT CATTTTCTTC    5160

TGGGAGGAGG ATAGTTTCTC TACCGTCCAT GTCTAAAACC AGTACTCTTG GGGGATAACG    5220

AGGGTCGAAA GGATGGTTAA AGTCAAAATC AATGGCTGTA GGGAGGTGTT GACTTGAAAA    5280

GTGGAAGGTA ATCTTTCCTT GGTTATTAAG CAATTGAAAC TCGAGTTCTT CTTCCAATTC    5340

AAAGACATTT TTTAAGAAAT GGTCGATGAT ATACCAAAAA GAGTCAATGA TGTCATCAGG    5400
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1298

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CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCATATC      5460

TCTGTCCCCT TTCTTTTCCC TTATCATACA GCAAATAGGA TTAAAAATCA AGAAAAGGTG      5520

ATTTTTTGAA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAATTCCT AAAAATCTAC      5580

CGAAGTTAAT AGGTAAATTC CCAAATTAAC TTGATTATAT AACTTTCAGT TACTTTGAGA      5640

AGTTACCGAA AAATATTTTT CATATCTATT GACTTTTAGG GGTAAAATTT GGTATGATAG      5700

TAGGCGGTAT TGTTTACCCC ATTTGAAAGG CCCCGGAACC TTCCAAATAC TTTTCGATGG      5760

GAAGGAACAC CCATCACCGT AAACAAAAAT CGAACTATAT ATAGGAGAAA TCATGAACAA      5820

AACAACATTT ATGGCTAAAC CAGGCCAAGT TGAACGTAAA TGGTACGTAG TTGACGCAAC      5880

TGATGTACCA CTTGGACGTC TTTCTGCAGT AGTTGCTAGC GT                        5922
```

(2) INFORMATION FOR SEQ ID NO: 268:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1988 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```
TAACTATCTA CGATGAGCTG TTGTGATTCT CATTAGTTCC CCTTTCCCAA GAGGCATAGG       60

GGTGCGCATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATTCCGTTC      120

CATTATCTGC CGTGATGGAA AGAATCTTGT GTTGTTTTAA GATGAGTTTT AGAGCCTGAT      180

TGACCACCTC AGCACTTTTA TTTGGAATCA ATCGGATGAT CTGATGTCTA CTCTTTCGAT      240

CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCGTA TCAATCTCAT      300

AATGCCCATT CTCCAAGCGA AGATTGATAG CTTCAGGCCG CTGTTCGATG GATTGACCAG      360

CAGGTTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTTT TCCTTTTCTA GGGTAAAGCA      420

AATCCTGCTT GCTTAACCCC AATTTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC      480

CCACGTTAAC CCCTTTAGCC ATAACCATCA TTTCAGGCGA AAATTTTTGG TTATGATAGT      540

GGAGAATCTT TTCCTTTAGT TCCTTGGTCA AGCTTGATTT CTTGACCGAG CGCTTGCGAT      600

TGTTTTCATA AGACTGTTGA GCGTAGTCGG CAGAATAAAC CTCTTTGAAG CGCCCTTTTC      660

CAAGACATTG TCGGACTGTC CCACGCTTGA TTTCAGTGTG ATAGTTTGAG GAGCTTTTCC      720

AAGTAGAGAG GCAATTTCTC TATTTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG      780

ACGGCTATCG ATTGTCAAAT GTTTGGCTTT TGTAGTATAA TTGTCTTGCA TCTCTGTGCC      840

TTTCTTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTTCTT ATGCCTACAA      900
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1299

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GAGCTTTCAT TATTTCCATT TTCTTTTGGA TTTCACTCTA TTCTGAAAAA CTTGTGTATA        960

TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG       1020

GGGAATCTCG GATTAATAGA TAGAGAGTTT TTAGTTTAAA TAAATTGTTT AAAATATCAA       1080

CAACATCACT TCTTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA       1140

TATTGTCCTC AATATCGTCT AGAAAGACAC AATTTCTAGG TTATAACTGG TATTTATCGA       1200

TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT       1260

ACCTCCATAC TCACCTTACA GATTCTTTTG GTAATAATAT CTTTGCCTAA TGTAGAGACA       1320

GTCTTGCAAA GAAAAAACTT CCTTGTAGCC ATGTTTCTGA TAAAAGTCCG GTGCCTGGAA       1380

CTGGTAAGTA TTGACAAAGG CAAAACAACA ATTTCGATTC TTAGCTTCAC TTTCTGCCTG       1440

TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGCAGTTCC TCTTTTACAA ACAAATACTC       1500

GATTTCTAGC CAATTTCCAA AAGTCTCTGC TATCAAACCT GCCAGGAGAT TGCCCTTTTC       1560

ATCTTCGACA TAAAGATTAA GTGGCTCACT TTCAGCCTCT TCTCTTTTTG AACGGTTATA       1620 .

AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA       1680

GTATAGTGAA ATGAAATAAA ACATGCGCAA ATCGATTAAG GAATTTAATC TAATTTCTAA       1740

CAATGTCTTA GAAATCAAAG TGTACTATTT TAACTTCAAT GCACTATACA TCTAATACTC       1800

AATAAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGGT TGCTCAAAAC ACTGTTTTGA       1860

GGTTGTAGAT AGAACTGACG AAGTCAGCTC AAAACATAGT TTTGAGGTTG TAGATGAAAC       1920

TGACGAAGTC GGCTCAAAAC ATGGTTTTGA GGTTGTAGAT GAAACTGACG AAGTCAGCTC       1980

AAAACAGG                                                                 1988
```

(2) INFORMATION FOR SEQ ID NO: 269:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 709 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```
CCGGATATTT GTTTTATGTA ATTTTCTTGC AAGTTTCTTC TTAGTAGCTT GTCAGTCAGG         60

TTCTAATGGT TCTCAGTCTG CTGTGGATGC TATCAAACAA AAAGGGAAAT TAGTTGTGGC        120

AACCAGTCCT GACTATGCAC CCTTTGAATT TCAATCATTG GTTGATGGAA AGAACCAGGT        180

AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACTTGGGG TTAAGTTGGA        240
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1300

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AATCTCAAGC ATGAGTTTTG ACAATGTTTT GACCAGTCTT CAAACTGGTA AGGCTGACCT      300

AGCAGTTGCA GGAATTAGTG CTACTGACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC      360

ATACTATGAA AACAAGATTA GTTTCTTGGT TCGTAAGGCT GATGTGGAAA AATACAAGGA      420

TTTAACTAGC CTAGAAAGTG CTAATATTGC AGCCCAAAAA GGGACTGTTC CAGAATCAAT      480

GGTCAAGGAA CAATTGCCAA AAGTTCAATT AACTTCCCTA ACTAATATGG GTGAAGCAGT      540

CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACTTAG      600

TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGGACGG      660

CGACGCCAAT GCCCGyTGCTC TTAGAAaATA GTGATGATTT GAAAGAAGT              709
```

(2) INFORMATION FOR SEQ ID NO: 270:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1680 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```
TATAAAATGT TAAGTTAAAT GATTTCAAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT      60

TTTTATTTTA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAAACTGAT     120

TGTGATGGGG CTATTCTAGC TTTAGAAACC TTCAAAAATT AAAATTTAAG GCAATCAATT     180

ACTTGGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTCT AGGTCTAGAA TTACATATAT     240

ATATTTATGA AGACGGGGTG TTCGATAGTT AGTATTGTTC TATTCTGAAA GATTTGAGCT     300

GTCAGTTGTA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATTGTATGAG     360

GTGCTTTATG ATATAATGTT CTTAATGAAT TTTCAGAAAG GAAAACCTCA AATTGTTCTA     420

CAAATTTCTA CTCTTCGACC TCGACCACAC TCTTCTTGAT TTTGATGCTG CTGAGGATGT     480

GGCTTTGACC CAACTTCTAA AAGAAGAAGG AGTTGCGGAT ATTCAGGCTT ATAAAGATTA     540

TTACGTTCCT ATGAACAAGG CTCTCTGGAA AGACTTGGAG CTGAAGAAAA TCAGTAAACA     600

AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG     660

TAGTTTTCTT GCCCAGCCGTT ACCAATTTTA CCTCGCCCAG CAGGGACAAA CACTATCGGG     720

CGCTCATGAT CTCTTGGACA GCCTCATTGA GCGTGATTAT AACTTGTATG CTGCGACAAA     780

TGGCATTACT GCCATTCAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA     840

TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG GATGCTCTTT TTTATGAAAA     900

GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT     960
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1301

AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC ACTATCTGGT ATAATCCTCA   1020

TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA GTCTATTCTT ACCAAGACTT   1080

GCTGGATTGT TTAGATAAAA ATATTCTTGA AAAGATCACA TTTTAAAGGA GACGAGCTAA   1140

TGACTACAAA AAAGCTAATA TTACTATTGA AGAGTACATT GAAATGTCTG AAGTTGATTT   1200

TAATGAAGCT GTTAATTATG AATTTACATC TGACACTTGT CAATTAGCAA ATAGTATTTA   1260

TCAATCTCTT TTTAAGTTTT TTGATAAGAA AAATTTCTCT GGCGATTTAA TTTTTACTTG   1320

GAAATCTCCA TCATTAGTCA AAGAAGGGGA TTATATTGGG AGAAGGGATT CACAAGTAGA   1380

TAATCTTAGA GTAATAGGAA ATATATTTCC GAATTATCTT ACTAATCGAA AATATAGCCT   1440

CAATATGAAT CGTAATGGCT GTATGGGAGA TTTTCCTCAT GACTTTTTTG ATATATACCT   1500

AGATCATGTA GCAAAATATG CCTACGAACA AAAAGTTAAT AATATTAAAG AGTATTATCC   1560

TTTAAAAAGA GCGATTTTAC ACCAAGAGAA TGCATTGTAT TTTCGATTTT TTTCTAATTT   1620

TGACGACTTT TTAGAAAAAA ATTATTTAAA GACTATATGG CAAGTTTCTA AAGAAACTCC   1680

(2) INFORMATION FOR SEQ ID NO: 271:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 598 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC GTAGTATnTG TGGTGCATAA ATGAGTGAAA AGAGGATAGA GAGGATGAGG   60

CCGATAAGAA CACCGGTAGC TGCATCGTGA AATACTTGTT TTTTCATACT TCTAATTTCT   120

CCTTGATGGT TTTTAGATAA CGGCGTGAAG AGTAGGTGAA GCTTTCGTTT TTCAAGAAAA   180

TTTCTACCAG ACCGTTTGGC GTGAgCTTGA GGTGAGAGAT GGAATCGATA TTGATGATTT   240

CTGATTGGGA AATTTGGATA AAATTGGTTG GCAAGAGTTT AAGAACCTGA TAGAGTCGCA   300

AATCAATGCT GTAGGTCTGA CTCGCGGTTT CTGCTAGAAC CTTCCGATTC TCGATATAGA   360

AGCGCTGAAT CTTGCCAATC TCAACTAGAT AGACCTGATC ATCGATTTTT CCTTTGATTT   420

TTTCTCTTTG GTCCAGATTT TCTGCGAACT CGATGACTTT CTGGACTTTT TCGGTTTCTT   480

GAGGTGCTTG GACAATCAGC TTTTCCTCCT CGTAAGTCTC ACTAATCTGT AGTTCTACTT   540

TCATAGTTTT CTCTCCTTTT CAGTTATACA AGGTTGTGAT CACTTCCTGT ATATCCGG   598

(2) INFORMATION FOR SEQ ID NO: 272:

1302

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1099 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```
CCAGCAAATC AATAACTGCA ATTGCTATAA AATGGATTCT ATAGAGTTTT TTCATGACAA          60

GACCTCCCTC TTTTATCTAA CTTCATTCTA CTCCAAAAGA ATGGGAGTTA CAACTAAAAT         120

GATAAAAATA GCAGAAGGGA GATTCTCTTA AGTTGGCTAG TATTCTTTAT TTGAGTTTCC         180

TTCTATTATC TAACTTCTTC ATCATTCCAG ACAAATAAAG CTCCGATTGC ATTGAGGATA         240

TAAAAGATGT ATTTACCGAT ATTGGCGAAG TTTCCTTGAA TACCAGCTTT TGTCAGCTGA         300

ACGAAATTGT AAATCAACCA AAAGCCCCAC TGAGTTGTTA GTTTTAATGC ATTCAAAGCA         360

TTGGCAATGA GGGACAGTGC AAAGGCAATA GTTGTTACGT AGGCAAGGAG ATTCATCTTG         420

CCCCCATATC CGATATAGTT GGTCACAAAG GCAAAGAGGA AGGCGATGAT GGAAATGATG         480

ATGGCCGCCA ATTTTACCTG TTTTTGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT         540

TCCCACTTCT TTATAGCAAA GGTATAAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC         600

GCCTTATTTC CAAGGATATA ATCAATAGCA CCGGACAAAA TGGTATTAAC AATACCAAAG         660

TAATTTCCCC ATTTGCTTAA TTTCCCCGTG AAACGAGTGG ACAACATGGA AATCCCAACG         720

TTGGTTACGG AAATCAATCC AAAGGGTACA AGAGCTGTCC ATGATCCCCA GTCTACAAAT         780

TTATCGAGGT GTGAGTTGAG GTAACCAGAT GCAATCGCAA TCCCAACGAC CAAAGCAACC         840

CCGAAGAGGT CAAACTATTT AGATGTAGCA AAAATTTTTA GTGATTTTTT CATAGGTTAA         900

ACTACCTTTC TTTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAAATAA AATGATAGAA         960

ATAAAACCCT GAAAATAAAG GTTCTATAAT ATTTGTAGTG GGTAAATCCA CTATAGATAT        1020

TATGGAGCCT ATTTTATTGT AGAAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA        1080

AACAACTCAT TAGAAAGAT                                                    1099
```

(2) INFORMATION FOR SEQ ID NO: 273:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2723 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

1303

```
CTGGGATTCA CGTGAAAAGG AAGCCCAGAG AGTAGCCAGG TGTACTGCTA GAACAGTGAG        60

TGAAATTGAA TATTACCATA GAGAGTCAAC CCAGATAGCT CAGGCTTTAG TTGAAAATCA       120

AGCTCGTATC GAGGGAATCT ATAAATACTT TAGCCTTAGC ATGCCAGACT ATTTTTACTG       180

GCAATTAGAG CGGAAAGCTT CGCCTTATAT ATCAGTCTCT CTGTATGAAA ATGTTGATGA       240

CCTCTATGTT CGAAATGATT TTGTAACTGG GGTGGCCATT GCTTTTCAAG ATTACAAGGA       300

AGTCTATGTT TCTACTAAAG ACAAACGTAG GkkAGAAAAA ATCAGGGCTG AGGATTTCAA       360

ACCAGCAGGA AATAGTTTTG CCATTCCAGT GTCAGATCCA GTGTCAGATC AAGACTTAGG       420

AGTGATTTAC ATCTCCTTGG ATCCTGCTGT TTTATACCAT GCCATTGATA ATACTAGAGG       480

TCATACTCCG ATGGCAGTAA CAGTGACCTC ACCTTTTGAT ACGGAGATTT TTCATATGGG       540

TGAGACAGTT GATAAGGAGA GTGAAAATTG GCTAGTTGGC TTAACTTCTC ATGGATATCA       600

GGTTCAGGTG GCAGTTCCTA AAAACTTTGT TTTACAAGGA ACAGTGACTA GCTCTGCTTT       660

GATTGTGGGT TTGAGCCTTC TCTTTATTGT CATTCTTTAT CTGACTTTGA GGCAGACTTT       720

TGCTAATTAC CAAAAGCAGG TAGTGGATTT AGTAGAATCC ATTCAAGTCA TTGCTCAAGG       780

CGAAGAGGGG CGTCGGATTG ACATTTCCGA GAAAGATCAG GAATTACTCC TAATCGCGGA       840

GACGACCAAT GATATGTTGG ATCGATTGGA AAAGAATATC CATGATATTT ACCAGTTAGA       900

GCTTAGTCAA AAAGATGCCA ATATGCGAGC CTTGCAGGCG CAAATCAATC CTCATTTTAT       960

GTATAATACG CTGGAGTTCT TGCGCATGTA TGCAGTTATG CAGAGTCAAG ATGAGTTGGC      1020

AGATATCATT TATGAATTCA GTAGTCTCTT GCGTAACAAT ATTTCCGACG AAAGAGAGAC      1080

CCTCCTCAAA CAGGAATTAG AATTTTGCCG TAAATACAGC TATCTCTGCA TGGTTCGCTA      1140

TCCCAAGTCC ATTGCCTATG GTTTCAAGAT AGATCCAGAG TTAGAGAATA TGAAGATTCC      1200

CAAGTTTACC TTGCAACCGC TGGTAGAAAA CTATTTCGCG CATGGTGTTG ACCACAGGCG      1260

GACAGATAAT GTGATTAGCA TCAAGGCTCT TAAACAGGAT GGTTTTGTGG AAATTTTGGT      1320

GGTCGATAAT GGTAGAGGAA TGTCGGCTGA AAAGTTGGCA AATATCCGAG AAAAATTAAG      1380

TCAGAGATAT TTTGAACACC AAGCCAGCTA CAGTGATCAA AGGCAGTCTA TCGGGATTGT      1440

CAATGTACAC GAGCGTTTTG TGCTCTATTT TGGAGACCGC TATGCCATTA CTATAGAGTC      1500

TGCAGAGCAA GCCGGTGTTC AGTATCGTAT TACAATTCAA GATGAGTAGA AAGGGAGAAA      1560

ATGTATAAAG TATTATTAGT AGATGATGAG TACATGGTGA CAGAAGGTCT GAAGCGTTTG      1620

ATTCCCTTTG ATAAGTGGGA TATGGAGGTC GTCGCAACAG CCAGTCATGC CGATGAAGCT      1680

CTAGAATATG TTCAGGAAAA TCCTGTCGAT GTCATCATTT CCGATGTCAA TATGCCAGAC      1740
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1304

```
AAAACAGGGC TTGATATGAT TCGGGAGATG AAAGAGATCT TACCAGATGC TGCCTATATC      1800

CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TAGTGTGGTG      1860

GACTATTTGG TCAAGCCTGT TGATAAGGTA GAGCTGGGAA ATCTGCTGGA GAAGATTGCA      1920

GGTCAGCTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAATT AGACGAGGCT      1980

GGATTTGTTA GTTATTTAGG GGATAAGGAG AATTGGTGGA TAGGTCTATC CAAGGAAAAA      2040

CAAGGTTCCT TCACCATTCC CTACTATGTC TTGGGTCAAG ACTGGCAGAT TTTCATTTCT      2100

GGCCACCCCC TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT      2160

GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCTTTTACG GTTCTGTAAA TCTGCAGCAG      2220

TCTGAGAGTC TCTTTGCCTA TTACGAACCG ATTTATAGGG TTATCATTCA GGGAAATCTC      2280

AATCAAATCG TAGAAGAGTT AAATCTCTTG GAGAAGGTAG TTCTTGAAAA TACACCTCGT      2340

GTTTCGATTA CTAAACAGCT TTTTATCCAG TTTGTCATGG ATGTTTTCCA TTTATTTGAA      2400

CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCATGCTAT TCAATCCTTC      2460

GATGAATTGG TTTCTTATAT CAAGGAAACT CTGATCAGCT TTTTCGGTCA ATACCGTATG      2520

AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC      2580

CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAAG      2640

CGTGAAACCG ATTCGACCTT TGCAGAGTTA CTAAACAAAC AACGTATTAA GGCTGCCCAG      2700

CAGCTCTTGC TTTCAACTAG TGA                                              2723
```

(2) INFORMATION FOR SEQ ID NO: 274:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 836 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```
CCGCAGTTTT TTTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAGAAT GCAAGATTTT       60

TGCAAACTTT TTTAAAATTT TTCGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA      120

CCTTGCTTAA CAACCTGTTC TCCGGCGATA TAAACATCAT CTACATCACT AGATTTAACT      180

GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTTGGA GATGAATTTT CCCTTGTGGT      240

TGAATGACCA GAAAATCTGC TTGCTTGCCG ACTTCCGACA TTCCTATCTG ATTTTCCATT      300

CCAAGGACCT TAGCCCCTTC GATTGTCAGT ACCTTGAGAG CTGTTTCGAT TGGAAACTGG      360

CTGGCATCCC CACTTTTCAT CTTCTGAAGA AGAGCTGCAG TCCTTCCTTC CTCAAACATA      420
```

1305

```
TCTAGATTGT TATTGGAAGC AACCGAGTCA GTCGCAATTC CGACTGCTAC TCCCGCTTTT      480

TGGAGCTGGA TAATTGGAGC AATTCCTGAT GCCAGTTTGA GGTTACTGAT AGGATTGTGG      540

GCGATAGCnA CTTGAGAAGA TGCCAAGCGT TCAATTTCTC TCTCGTTTAA TTCGACCCCG      600

TGAGCAAATA CGGACGGATG ATCTAAATAA CCCAGTTCTT CAAGAAAAGC AAGGGGGCGT      660

TTGCCGTATC GTTTGAGGAT AATTCCTGAC TCCTCCTTGG TCTCCGCCAC ATGGACATGG      720

AGCGGAATAT TTAGCTCTTT TGCCATTTCC AAACTCGCTT CCAGCAAGTC TCTACTGCAG      780

CTATACGGAG AATGAGGTGC TACCATAACC TTGAAATTTG GATTTTTATA TTTTAA         836
```

(2) INFORMATION FOR SEQ ID NO: 275:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2335 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```
ATTTTATTTC ACTTTTTAGG TGGTCTGGGG CTATTCTTAT ATAGCnTCAA GACCATGGGA       60

GACGGTTTAC AACAAGCTGC TGGAGATCGC CTGGGTTTTT ACATTGACAA ATATACTAGT      120

AATCCTTTGT TTGGAGTTCT GGTTGGTATT GGGATGACTG CTCTAATTCA GTCTAGTTCT      180

GGTGTAACAG TTATCACAGT CGGCCTGGTC AGTGCCGGTC TCTTAACCTT ACGTCAGGCT      240

ATCGGGATTG TCATGGGTGC TAATATTGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT      300

AAATTAGGTA ACTATGCCCT ACCTATGCTC TTTATCGGTG CCGTCTGTCT TTTTTTTACG      360

AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCTTTG GTGTCGGTGG TATCTTTTTT      420

GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACAGGT CTTTAAGGAC      480

TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTGTCT TTGTCGGTAC TGGCTTGACC      540

TTGCTAATTC AAGCTTCTTC GGCTACCATT GGGATTTTAC AAAACCTCTA CGCCGGCAAT      600

CTAATTGATC TACAGGGAGC TTTGCCAGTT CTATTTGGTG ACAATATCGG GACAACCATT      660

ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATTGCAGCTA AACGGGTAGC AGGAGCTCAT      720

GTTGCCTTCA ACGTTATCGG AACAGTTGTC TGCGTTATTT TTCTAGTTCC TTTTACTGTC      780

CTGATTCATT GGTTTGAAGC TACGCTAAAT CTAGCACCGG AAATGACCAT CGCCTTTGCT      840

CACGGAACCT TTAATATTAC CAACACCATT GTCCAATTTC CATTTATCGG AGCTCTGGCT      900

TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTTG TCAAATACGA ACCCTTATAT      960
```

1306

```
CTTGATGAAC ATTTCATCAA ACAGGCCCCA TCTATCGCTC TAGGAAATGC TAAGAAAGAG    1020

CTCTTGCACT TAGGAAACTA CGCTGCTAAA GCCTTTGACC TTTCCTATAA GTACATCATT    1080

GACTTGGATG AAAAAGTTGC TGAAAAAGGG CATAAAACCG AAGAAGCAAT TAACACCATC    1140

GATGAGCAAT TAACACGTTA TCTCATTGCC CTTTCAAGCG AAGCTCTCAG CCAAAAAGAA    1200

AGTGAAGTGC TTACCAATAT CCTTGATTCC TCCCGTGATT TGGAACGGAT TGGAGACCAC    1260

ACGGAGGCTC TACTCAATCT GACTGACTAT CTTCAACGGA AAAATGTTGA ATTTTCTGAT    1320

GCCGCCTTGA AAGAATTAGA GGAAGTTTAC CGCCAAACTA GTGACTTTAT CAAAGATGCT    1380

CTGGATAGTG TGGAAAACAA TGATATTGAA AAAGCACGCA GTCTTGTAGA ACGTCATGAA    1440

GCAATCAATA AGATAGAACG TGTTCTCAGA AAAACCCACA TCAAACGCCT CAACAAAGGC    1500

GAATGTTCAA CACAAGCTGG GGTCAACTTT ATCGACATCA TCTCACACTA CACTCGTGTA    1560

TCAGACCACG CTATGAACCT TGCTGAAAAG GTTTTTGCAG AACAAATCTA AGAACCAAGA    1620

AGCTATCCAT CATAATTGGA TGGCTTTTTA CTTTTTCCTA AGCAAGACTA GGATGAATGA    1680

AACTGAAAGA GTATTCTGCA GATATATAGT CCCCAATTAT TCACCCCAAA TCTAAAAACC    1740

ATCCAGAATC CTTGCCTTAG CTTAGATCCT GGATGGTTTC TTTTTTCACC CAATGGGTGT    1800

TTTTTACTAG ACAAAAAAGA GTTTCCCCTT TATGGTATAA GTGTAGAAAA AAACACAAAA    1860

AGAAAGGAAA CTCACATGAA CAGTTTACCA AATCATCACT TCCAAAACAA GTCTTTTTAC    1920

CAACTATCTT TCGATGGAGG TCATTTAACC CAGTATGGTG GTCTTATCTT TTTTCAGGAA    1980

CTTTTTTCCC AGTTGAAACT AAAAGAGCGG ATTTCTAAGT ATTTAGTAAC GAATGACCAA    2040

CGCCGCTACT GTCGTTATTC GGATTCAGAT ATCCTTGTCC AGTTCCTCTT TCAACTGTTA    2100

ACAGGTTATG GAACGGACTA TGCTTGTAAA GAATTGTCAG CTGATGCCTA CTTTCCAAAA    2160

TTGTTGGAAG GAGGGCAGCT TGCTTCACAG CCAACCTTAT CCCGTTTTCT TTCCAGAACT    2220

GACGAGGAAA CAGTCCATAG TTTGCGATGC CTCAACCTTG AATgGkCGAA TTCTTTTTAc    2280

AGTTTCACCA GCTAAACCAA CTCATTGTAG ATATCGATTC TACCCATTTC ACAAC         2335
```

(2) INFORMATION FOR SEQ ID NO: 276:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 752 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```
CGGATTCACT GTTGTTGACT AATCAATAAC ACAGTAGAAA ATCTCACAGC AGTCTATTAG      60
```

1307

```
TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG GGTACAGCAA GGGAGCTTAA    120

GGCCGTAGAA GAGAAAAATA GTAGACTGAA AACCCGCAAG ACTTCATCAT TTCGAGAAGT    180

GACGTGGGAG ATGAAAATCG ATTGAACCAC TTACAAGGAG AATAGAAAAT GGCTAAAAAA    240

AGCAAACAAC TTCGTGCTGC TCTTGAGAAA ATCGACAGCA CAAAAGCATA CAGTGTAGAA    300

GAAGCTGTAG CACTTGCAAA AGAAACTAAC TTTGCAAAAT TTGATGCAAC TGTAGAAGTT    360

GCTTACAACT TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCGTGG AGCAATGGTA    420

TTGCCAAACG GTACTGGTAA AACTTCACGT GTTCTTGTTT TCGCACGTGG TGCAAAAGCT    480

GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGCTAAAATC    540

AACGACGGTT GGTTGGACTT CGACGTAGtT ATCGCTACAC CTGATATGAT GGCTCTTGTT    600

GGACGTCTTG GACGTGTCCT TGGACCACGT AACTTGATGC CAAACCCTAA AACTGGTACT    660

GTAACAATGG ATGTTGGCAA AGCGGTTGAA GAGTCTAAAG GTGGTAAAAT CACTTACCGT    720

GCTGACCGTG CAGGTAACGT TCAAGCAATC AT                                  752
```

(2) INFORMATION FOR SEQ ID NO: 277:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2643 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
GTCAACATTG ATTTCAAGGC TGTTTGCTTT CTATCTCCCC TTTTTCATAA TGTATAATAA    60

AATGAAATAA TAACAGGACG AATTGATCGG GACAGTCAAA TCGATTTCTA ACAATGTTTT    120

AGAAGTAGAG GTGTACTATT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC    180

CATTTGAACG ATTTCAAATC CTTCTTTTTG GTAAAGATTC TGAGCTCTTT GATTTGCCTC    240

GAAGACATTT AGAGAAATAC TGTCTATATC TCTATTTTCA AATGCTAAAC TAACAAATTT    300

CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTTCTGG GGGTTGATAA AAAATCTCCC    360

GATATGAAGA TTGCTGTCTT CTAGCCTGAT TTTCTGGATA AATCCCACAA ACTCTTGTTC    420

ATCAAAGATT GAAAAGACTC CTTCCAAGGC TTGAAGTGTC AGTAGAAAAG GAATCCTTGG    480

TCCCATCCAT TGTTCTTGAA AGGATTTGCC TAGGGAGTTG GACCACTGGC ATACAAATTG    540

AGCGTTTTCT GTGCTCACCT TTTCTTCAAA ACGAATTGTC ATCTTTTCCT CACCACCTTA    600

TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTTTACG AATAGATAAG TATGATTGAT    660
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                                        1308
TTTTATTTTT TTCTCGTCGG GAGCATTCTA GCTTCCTTTC TTGGTTTGGT CATTGACCGT      720

TTTCCAGAGC AATCCATTAT CAGTTCAGCC AGTCACTGCG ATTCCTGTCA GACTCCCTTG      780

CGTCCCTTAG ATTTGATTCC GATTCTCTCA CAGGTCTTCA ATCGCTTTCG CTGTCGCTAC      840

TGCAAAGTTC GCTATCCTGT CTGGTATGCC CTCTTTGAAT TAAGCTTAGG ACTCCTCTTT      900

CTGCTTTACT CTTGGGGATG GCTCTCCTTG GGGCAAGTCG TCCTAATCAC CGCTGGTTTG      960

ACCTTGGGTA TCTACGACTT TCACCATCAG GAATATCCCT TACTGGTCTG GATGACTTTC     1020

CAGCTAATCC TAATAGCTTC CTCTGGCTGG AATCTGGTCA TGGTCTCCTT CCTCATACTT     1080

GGAATTTTGG CTCATTTTAT CGATATCCGC ATGGGTGCAG GGGATTTCCT CTTTTTAGCT     1140

TCTTGTGCTC TCGTCTTTAG CGTAACGGAG TTACTGATCT TGATTCAGTT CGCTTCTGCG     1200

ACGGGTATCC TGGCCTTTCT CCTGCAAAAG AAAAAGGAAA GACTTCCTTT CGTGCCTTTC     1260

CTCTTACTTG CTACTTGTTT GATTATTTTT GGTAAGCTAC TGCTTGTCTG ATAAAATCCA     1320

ATTTCTGCCA TATATCCTTC ATGAAATTAT TTCACAGTTA AATTATAAAT TATTTCTTTT     1380

GTACAAAGGG ATGATGTTAT CAAATCGATC TGTTCTTCTA TCTTCTTGAT ACTGATCAAA     1440

AAATTTCATT TCGACTGAAA ATATTTCGCT TATAAACTGT AAACGAATAC TTTGTTTAGA     1500

CATTATAGTC GCTAGACTGA CTAGATGATT ACTCAAAACG ACGTCCAGAA TACTCTTTAC     1560

TTTGCTTGGT TTTTTAACAA AAATTTGATC ATCCAAGGGT TCAATCATTT TGTAACCTTT     1620

TTGCGCAATT TGACGATAAA AGTAAGAATG TTGCTTTGGA GTCAATAATC CTAACTTAAA     1680

AGCTCGATAC TCTAAAGCCT GTATCGAAAC ATTCAAATCC GACTTCAATA AAATATAACT     1740

ATCAGGATTG CTGACACGCT TGCCAACCCT CTCTTCAAAT TTGACTAAAA ACTCTTCTTT     1800

TGGCAATAAA AAACATGATG CAAAATAATT TGCTTCTTGC TCCAAACGAT CGCCATCTTC     1860

ATTCATATCT TTATATTTAT GTAAAAGAAT ATGTCCTAGC TCATGAGCTA AGTCAAAATT     1920

TCGACGTACA GATGATTTAT TCGTTCCTAA CACAATATAA GGTCTTCCCA ATTTTGACCA     1980

TGCGCTATAA GCATCAGCTT GGCCATTAAT TAATCGTTCC ACGATATAGA TGCCTGAACG     2040

TTCTAATTTA TAAAGCAAAT CATGATTATC TTTTGAAATA CCTAATTTTT CCCTGGCATA     2100

AAGAGCCAAT TCCTCAATGG ATTCTCCCTT ATGATAAGAT TCACTCACTA CATTACTTAG     2160

GTCATGAATT ATAATATTAG GTATAATTAC AAAACTTTCA AAATAATCAA TCAAACTATC     2220

TACCTTATGT AAATACATAG TTTGAATATC TATTGTTTTC CGTGTTGCTA GGTCTGCATT     2280

TCTAAAGGCA ATTACAGAAG AATCAAATCG AATGCTCTCT TCTTCCTGTT CAAAATAAGT     2340

TAAATCAACA TGAAATTGGT TGGCCAAATG CATTTTGGTT GATAATTTAG GTTTCGTTTC     2400

GTTGGACTCA AACTGCCAAA TGGCTTGTTC CGTTAAATTA ATTCTCTGAG CTAATTCTGC     2460
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1309

TCTACTTAAA CCATTTAACA GCCGTAATTC TTTCAATACC CGACCATTAA ACATTTACAT   2520

ACTCCTTACT ACTTTTGACC TTCTTGTTTT TCTATTCTTG GAATAATTTC AAAATCTTCT   2580

GTTTCCGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC   2640

GGG   2643

(2) INFORMATION FOR SEQ ID NO: 278:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 582 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAGTGG CAAAATGGCT ATCCAAATGC AGATGTTATT ATCGATGATA TCATCTCAGG   60

GCAAGCCTAC GTAGCCTTGG AAGAGGGAGA ACTGCTAGCC TATGCTGCTG TGACCAAGAG   120

TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAAACTGG CAAGCTGGAG AGTCAGAGTA   180

TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATGTGCAG GGAAaAGGAG TTGCTCAAAC   240

CTTCTTAGAG GGCTTGATTG AAGGTTTTGA TTATCTTGAT TTTCGCTCAG ATACGCATGC   300

TGAAAACAAG GTTATGCAAC ATATTTTTGA AAAACTTGGT TTTAAACAAG TCGGTAAGAT   360

GCCAGTAGAT GGCGAACGCT TGGCCTATCA AAAATTAAAG AAATAATGCA AAAGAAGTAT   420

GTAAAAATCC TCTACTCCTC ACCAATTGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT   480

TTGTATGGAA TTTGGGTTCA GGAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAACG   540

ATAGAAGAAG TTGTwAGTCA TCCTATTTTA GACCCAGTTA TT   582

(2) INFORMATION FOR SEQ ID NO: 279:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 554 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AAACTTGCTA GAGAAGCAAG AGAAAGTGTG AATCTTTTTA   60

ATTTCATGAT GAATTTCCTT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT   120

CCCCTAGTAT AACAAGTTCA AAAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA   180

1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCCTGTAACG AACAGCAAGT CTTGAGCGTC   240

TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGGTAAGAA GAAACTATAT CGTAACCTGT   300

CACATCCCTT TCGTCCAAAG CCCCCTGATA GTCAAAGCCG GTCACCTTGA GTTCCACCTG   360

AGGCAATTTT TCAGTCAGAT AACCCAACAT CCCTTGATAA TCCTTACGTT TCAAGGATCC   420

AAAGAGGATT TGAGGTCGAT AGCCTTCCTG CTCTTTTTCT TTGATAAACT CAGCCAAGCG   480

AGTCAAGGCA GGGAGGTTAT GAGCACCATC CAAATAAATC TGTGGGCGAA TACGCTCCAA   540

GCGAsCAGCC CAAT   554

(2) INFORMATION FOR SEQ ID NO: 280:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 766 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AAATGAATTT CTTGGTTGTG GCTAAAAAAT ATGCTACACT ATCAATATGA   60

AAATTTTAAT CCCAACAGCA AAAGAAATGA ACACAGACTT CCCAAGTATC GAGGCAATTC   120

CTTTAAAACC AGAAAGTCAG GCCGTGCTTG ATGCCTTGGC TCTCTATTCT GCCAGTCAAT   180

TGGAGAGTTT CTACAAGGTA TCAGCTGAGA AAGCGGCGGA AGAATTTCAA AATATCCAAG   240

CTTTGAAAAG GCAAACTGCT CAACACTATC CAGCCTTGAA ACTTTTTGAT GGGCTTATGT   300

ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGGCGGAACA AGATTATCTT GAAAATCATG   360

TTTTCATTAC CTCGGCTTTG TACGGTGTTG TTCCAGTCTT GTCACCCATG GCTCCTCACC   420

GTTTGGATTT TTTGATGAAA TTAAAAGTCG CTGGTAAGAC TTTGAAGAGC CATTGGAAGG   480

CAGCCTATGA TGAAACTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTG TCATCAGAGT   540

TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAAA TTCATGGAGG   600

ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCGCGC GGGGCCTTTC   660

TAACAGCTTT AATAGAAAAT CAAGTACAAA CTGTGGGGGa AGCACGTCGC TTGAACTTTG   720

CTGGATTTGT TTACCGAGAA GATTTGTCAC AACCACAGGG GGATGG   766

(2) INFORMATION FOR SEQ ID NO: 281:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 901 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```
CCGGCCACGG TTCCATCCAA CTTCACAGGT GTGCACTTGA TTGTGTATGT AATTGTCACT        60

AACGGTAGAA TTTCACCTAT CCCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCTGAAAG       120

AAGAAGATAA CCTACTTATC CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTTGCAAA       180

TAGATTTTTA AATTTTTGGC TAATTGTCTG AATCAGGGTC GGAAGTTTGA CGACCTTGTC       240

ATTGCCTAGT TTTTCGCGTG CAATTTTGAG AATGGCACCT GAGTCTTTTG AAGCAAAGAG       300

GAATTTTCCT TTGTCTGTAA AGACTTCGAA GTGGCGGCTG ATTTTGCGTC CAGTGACATT       360

GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTCGA CATTGACATC       420

TGGGTAAAAT TCCAAAGCCT GATCTCCGAC AAGGAATTTC CCAACTTTCC CAGCGATAGA       480

GAGGTAGGAA GTGCCTGTCG TACTGAGGAG TACTGTTTTG TTAAGTGATT GGGCCATGCT       540

TAGTCTTCCT TACTTTCTCC AAAAAAGGCA TTGTAGAGGG CTTTAATTGC TGCTTTCTCT       600

TGGTCTTTAT TGACAACAAA CATAATAGAA ACTTCACTAG AACCTTGAGA CATCATCTGG       660

ATGTTGATTT TGTTTTCAGA TAGAGCGCGT GTCGCAGTAG CAGTCACTCC GATATGGCTC       720

TTCATTTTTT CACCAACAAT CATAATGATA GAAAGGTCGT GTTCGATTTC TGCATGATCT       780

ACTTTAGCCT TTTGAACCAA CTGACGCAGG ATTTCTTCTT CCTTGATGGG AGTTAGTTGG       840

CGAGAACGGA GAATGATAGA AAGAwCGTCG ATACCTGTTG GCATATGTTC CCAACCGATG       900

T                                                                      901
```

(2) INFORMATION FOR SEQ ID NO: 282:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1765 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```
CCCTGTTACG TGGATAATAG GGTAAGACTG CTCAGGATTT CCTAACAAAT CCACCGCTTG        60

CTGCATTCGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATTCTTC       120

TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG       180

TTACTAATAA AAACAAGGCC AGGATTTTCG TCCCGACCTC TTACCTGGTT AGCTAATAAC       240

TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGACGTTCCA ACTCTTCCCC       300
```

1312

```
ATTTCTGGGA GTTGGGGTAA AAATGTTCAC TGGACGTTCC AACTCTTCCC CATTTCTGGG     360

AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACTCCTCC ATAAAGCTGT TGAAGACTTC     420

TTCAATCATG TTCCATTCGT CTTCTGAGTC TTCTGGGATT GGTTGCAATT CGCCTTCTGT     480

TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGATTTCA ACTTGTCCGT CTTCGTCTTC     540

TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTTACCA AATTCTTCTT TTCCATCAAT     600

TGTCAAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGATTAGTTC     660

ACGTTCTTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTTAT ATTAAAATTT     720

TCTATCTAAA TAATTTTGTA AAATCAGCTG AGCTGCTAAC TTATCAATGA CTTTCTTGCG     780

CTTATTGCGA CTGATATCTG CTTGTTCAAT CAACATGCGC TCAGCAGCCA CTGTTGTCAA     840

GCGTTCATCC TGATAGTCTA CTGGTAAACC AAAAAACTCT TCTAGCTTTG CTCCGTAGCT     900

TGACTAGCTT CTACGCGCGG TCCACTTGTA TTGTTCATGT TTTTAGGCAA GCCCACTACA     960

AATCGTTCCA CCTTGTAAGT ATCAACCAAT TCCTTAACGC GGTCAAAACC AAATTGGCCT    1020

TGTTCTTCAT TTATCTGGAT GATTTCAAGC CCTTGAGCTG TAAAACCAAG CGGATCGCTA    1080

ATCGCCACCC CTACCGTTTT TGAACCGACG TCCAATCCCA TAATTCTCAT AGGTTATAGA    1140

TCGACTCCTT GTCCTTTGAG GTAGTAGCGA ACCAATTCCT CAACGATTTC ATCACGCTCA    1200

TACTTACGGA TTTGATTTCG TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC    1260

AATACGTAAC CTACGATTTG GTTAATTGGG TTGTAaCCCT TATCGTTCAA CGAAGCATAA    1320

ACATCTGTCA AAGTTTCGCT AATTTCTTTT TTATTGGAAT CGTCCAATTT AAAACGTACT    1380

GTTTCTTCAG TAAATCCCAT TCTAACACCC TCTTTCCTTA GAATAGTACC ATTATAGCAT    1440

AATTCCTTAC CTTCTACAAT TCAGGCAGTC TATTTATTTG GATTTTCTAT TGTTCTGTCG    1500

CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTTCAAA AGATTTTCCA    1560

AACCAATATT CTTCAGATGT TCCAACTGGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT    1620

CAAAACTAGT CGTTGTTTGA AGTTCCGTTG CGCTCAATAG TTTTGTTTCA AGTTTGAAAC    1680

CTGCCAATTT ACGAGCTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT    1740

TTTGAGTTTC CTCCACTCCA TGTTG                                         1765
```

(2) INFORMATION FOR SEQ ID NO: 283:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1346 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```
CTTATCCATT CACTTTCTTG TCTGTTATTC TATAAATCTT ACTCCTAAGT ATACCACATT      60

TGCCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGGT     120

ACAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC     180

GTTTCCTATC TGAAAAATGG TATCGAGTCT GGACGATTTC CGACGGGTAG TCGCCTGCCT     240

TCTATCCGTC AACTGAGCCT TGACTTTCAC TGCAGCAAGG ACACCATTCA ACGAGCCCTG     300

CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA     360

GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT     420

GACGATTTCC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAAACTA CCTCTTCAAC     480

TACTATGACA ATCAAGAAGG ATTAGAAGAC CTAAGACAGT CCATTCACAA ACTCCTCTTT     540

GAGCAAGCTC TCTACTGCAA GGCTAACCAA CTAGTACTGA CTTCTGGAAC CCAACAAGCC     600

TTGTTTATCC TCTCTCAAAT ATCCTTTCCT AGACAAGCCA AGGAAATCTT GGTGGAACAG     660

CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAGG GGCTGGACTA TCAAACGATT     720

GAACGAGGCA TTGATGGGAT TGACTTGGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA     780

ATTAAGTTTT TCTACACCAT TCCCCGATTT CACTATCCCC TGGGACATTC CTATTCTGAG     840

CAAGACAAAC GATCTATTCT TAACTTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC     900

GATTATCTGG GTGATTTGGA CTCCAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG     960

GAGCGTGTCA TTTATATCAA GTCCTTCTCG ACCAGCCTTT TTCCTGCCCT TCGTATTACA    1020

GCACTCATTC TTCCAAATGC TATCAAAGAA GCATTTGTGG CCTACAAAAA TATCCTAGAC    1080

TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATTGACAG TCAATTGTTT    1140

GAAAAAAATC GTTTGGCTCG CTTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA    1200

AGGATAACTA AAACACCTTG TCCCCTTCCT CATTATTCCC TACACGATGG yTTATTGCTA    1260

GACCTGAGAC AGTATCCTAA AATCGCCAGT CTCAAACACA GTCAACTGGG cTTGGACTTC    1320

TTTGAAGAGG CCTATTTAAG CACCTG                                        1346
```

(2) INFORMATION FOR SEQ ID NO: 284:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 900 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

1314
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```
CTATATTCAG AATATGCCAA AAAATTCGGAA TGGTATAAAT TTGCGGAGGG TTCATTTGAC        60

ATATTTAGAA AACTCCCCCA AAGAATTAAT TTTAAGAAAG ATTTTTCTAG AATTTTGGCC       120

CCCTTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAATAA AGAATACGAG       180

TGGATTGACA AGAATGGAAA TATTTTTTCC TCTCTAGTAT TTTATTTAGA AGATTTAATC       240

TATCCTTGGA TTGTTAAACC TTTGGTTTTA GAGATAAATT CATTGCGTGA AAAAGGTTTA       300

CTTGAAGGGG AATCGGAGCA GCAACGGTAC AAATATTTTA TAACATTGTT TGACAAGGAA       360

GAGAATATAT TAAATTTTTA TAACAAATAT CCCGTTTTAC TGAGGCAAAT ATCGGAGTCT       420

TGTCTTCGGT TCTATACTTA TTTTATAGAA ATTTTATCAA ATTTAGAAAA TGATTTTAGT       480

GTGCTAGAAG AAGAATTAGG GCTAAGGGGG AAATTAAATG ATATAAAATT TGGAAAGGGT       540

GATACACACA GCCAAGGAAA AACTGTTTTG ATACTCTTCT TTGATGACGC GAAAATTGTT       600

TACAAGCCTA AAAATTTAAT AATCAATAAC TCACTAAATA CTATTGCTGA GTATATCCGA       660

AAGGTTGATG AAAAAAATTAG GATAAGAATA CCTCGAACTA TTGCTTATTC GGATCACAGC       720

TATGAAGAAT TTATTGATTA TCTACCTCTA GAGCAAAAGA AAAATTTACC TGAATATTAT       780

TATAATTTTG GTGTGCTTTT AGCATTTATA TATTTATTTA ATGGGAGTGA TATACATTTT       840

GAAAATTTAA TTTCCTATGG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG       900
```

(2) INFORMATION FOR SEQ ID NO: 285:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 862 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```
TTATTTAGCA GAGGCAGTTT TAAATGTGAA GGATTTGGTC AGTCAAACAG TTTTTTATCA        60

GCAGATTATT GGTTTAGAAA TCCTATCTCA AACGGATACA GAGGTCGTTC TGGGACTTGG       120

AGGAAAAGCC TTGGTACACT TGATTCAAGC ACAAGAGGGT GGAGAAGTAA GGGAACATTA       180

TGGTCTTTAC CATCTGGCTA TTCTTTTGCC GACACGAAAG GCTTTGGCGG ATGTCTTGAA       240

GCACCTGACG GATTTACAGA TTCCTCTTGT TGGCGGTGCA GATCACGGTT ACAGTGAGGC       300

CCTTTACTTA GAGGACTTGG AGGGAAATGG CATTGAACTC TATCGAGATA AGCCAGTTTC       360

CACATGGGAT ATTCGAGAAG ATGGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA       420

GGATATCTAT GAGTTGGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAGG GTACGAGAAT       480
```

1315

GGGGCATATT CATCTTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTTT ATCAAACGGT   540

GTTAGGGCTC GAGGATAAAT TCAGTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA   600

CCATCATCAT TTAGCAGTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT   660

CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAAGAAGAAC TGTTAACGAT   720

TGCCCAACGA GCACAAGAAG TTGACGCACC AATCAAATGG ATGACATCGA TCCAATTGGA   780

AATCACAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA   840

TGAAGGTAGA GCATCAATTG TA   862

(2) INFORMATION FOR SEQ ID NO: 286:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 650 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCGCGAC CACGAATTCC AAGATAGCAC   60

GCGCTACCTC AATCATAGAT AGTTCACTTT TTTCTTGCCC AGCAAATACT TCTAATTCCA   120

AAGCGTTTCT CCTCATTTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA   180

TCATTTACTC TTTATTTTAC GATAATTTTG CGGAATAGTC AAAGGTTAAG GGGGAGAAAG   240

TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCTT TTTCTGTTGC TCCATTTTCC   300

ACAAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT TGTAGGTGTA GATTTTCTTG   360

ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCAA TCAAAGCACT TAGAATCTTT   420

TTTCCAAGTC CTCGATGTTG GTAAGCGGAA TTCCCAATCA CAATGGGGAG ATTATCCTGA   480

GATAGTGTAA TATCCCCAAT TGGAAACCAT TCTCCCTTCT CCTTGACTTC AATCCAAAAA   540

AGCTCACCAT GCCGATyCAr ATAGGAATAC ATGGCTTCCA AGGTCGcTtG ACTGTAAGGA   600

AGCTTCACCC CATCTACGAG GtAAcCAAGT TCACATCCGT GATACCAAGC   650

(2) INFORMATION FOR SEQ ID NO: 287:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1119 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

1316
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

```
GATAGCAATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG      60

AAGATACTTC CATTCTCATA CTATCTGTTG GCTTTGCAGG CTGTAAAAAC AACTTTTCTC     120

TTGCTACTTC CTGAAAATCT GAATCTTGCA GTTCTTTGCT TTCAAAATAG TCCTGTACTC     180

GCTCCACATC AAAATTCCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAAACTTTG     240

TAAAATTTTC TTGCAAATTA GTTAGATTGA TTTGGGAAAT GGACTCCTCA CTTCCAACTA     300

TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTCGCTAA AGTTGAAAAG AATAAACACG     360

AATCTGGATC ATCTTGGTAC ATTTCTCGTT CTTGCTGAAT AATATCCTGC TCTGTCAGAA     420

TGGAAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTCATC AAGTAAATCT AAATTTTCTA     480

AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTTGT AAAGCTTGTA AAGGCATTAC     540

TATCTGCACC TAGACTCGTA AAAGCCGACA TCAAATCACT AGAATCTTCT CTCTCAAATA     600

ATTTATGTTC AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT     660

CTGTGACAAA CGTATCTACC GAACCAAACT GTACAGTGAC ACTCCCGTAA ACCTCTTTAA     720

ATTCCTTTTT AGGCAAAAGA GCAACTGTCA ATCCGTTGGC CAAACGAGTT CGATAAACCA     780

TTTCTTTTAC AGCTGGATAG TATTTTTCTT CAAAAACAAC CTTTGTCATT CTATTCCTTC     840

CATAAAGTAA ATCGCTTGTA GTTTCACATT ATTAGCTACT CTACAAATAG CATCTTTGTC     900

AATTTGTTCA AGCTTTGCAA TCCAACTTTT AAAGTCTGCT GAAGATTTTC CAAATAAGGC     960

ATTTTGATAA GCACGTTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA    1020

ACGAATCATT TCCTTGGTCT GATTTAACTC AAACTCTGTA AAAAAACCTT TTTTTAAATC    1080

AAGCCGTTGA TTATTCATCA ATTTACGAGC CTGGTTACG                          1119
```

(2) INFORMATION FOR SEQ ID NO: 288:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 540 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```
ACGCCCTCGC GGGGACATGA CGAATTCCCC GTTCATCACG AAGGCCGCCG AGGAGTGGGG      60

GGTGCCGTCC AAGTCAAAAG CGGCCCCACA TCGATTCAGT TCCCCGACGA ACAGCCCTTT     120

CCCCCAGCGT TCCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGGACAA     180

GGCAGACGGA CTCCAAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCG     240
```

1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATTCTCCTC   300

AAAAGTGCGC AACGTCGCCC TGAATGAATC CTGCCTTGTA GTCGTGACCA TTCCTATGAA   360

GGGTCGCAGA GGATTTTCCC CGAGTGCAAG CGCATCCTCC GGCTCAAATC GGGTGCATTT   420

CACAGTCCCG CTCAACGCTA GCCCGATCCC TTTTTGGCAT GGTGACTCAA GCGTCCTTTC   480

AAACAAAAGC TCCTCATCCG CTCCAACCGG CCCGACGTAG ACGCGTAGAC CGAAGTCGTC   540

(2) INFORMATION FOR SEQ ID NO: 289:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1949 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAATTCG ACCAATTCAA GGTTGAGGCA TCGCAAACTA TGGACTGTTC CCCCGTCAGT   60

TCTGGACAGA AAACGGGATA AGGTTGGCTG TGAAGCAAGC TGCCCTCCTA CCAACAATTT   120

TGGAAAGTAG GCATCAGCTG ACAATTCTTT ACAAGCATAG TCCGTTCCAT AACCTGTTAA   180

CAGTTGAAAG AGGAACTGGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG   240

GTCATTCGTT ACTAAATACT TAGAAATCCG CTCTTTTAGT TTCAACTGGG AAAAAAGTTC   300

CTGAAAAAAG ATAAGACCAC CATACTGGGT TAAATGACCT CCATCGAAAG ATAGTTGGTA   360

AAAAGACTTG TTTTGGAAGT GATGATTTGG TAAACTGTTC ATGTGAGTTT CCTTTCTTTT   420

TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAAACTCT TTTTTGTCTA GTAAAAAACA   480

CCCATTGGGT GAAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGGT   540

TTTTAGATTT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG   600

ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCATAATTA CCTCCGAAAC   660

ACAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCCGAAA GTTTATTAAA ACAAAAATCC   720

TGCCAAAGAA TTTTTGGCAG GAAACCAAAT CAATTTATCA GTTCTATCA ATCGCTTATC   780

GCTCTCAAAG ACTGGTAAAT AGGGATTCCG CAATCAAATT GCGATACTCT ATTATTTAAG   840

AGTAACTGAA GCTCCAGCTT CTTCCAATTT AGCTTTGATT TCTTCAGCTT CTGCAGTTGC   900

AACGCCTTCT TTAACAAGTG CTGGTGCACC GTCAACAAGT TCTTTAGCTT CTTTAAGACC   960

AAGACCAGTG ATTTCACGTA CAACTTTGAT AACGCCAACT TTTTTGTCGC CTGCAGATGT   1020

CAATTCAACG TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAGCAAC   1080

1318

```
AGCTACAGGA GCAGCTGCAG TTACACCAAA TTCTTCTTCG ATAGCTTTTA CAAGGTCGTT     1140

CAATTCAAGG ATTGAAGCTT CTTTAATTTC AGCAATAATG TTTTCAATGT TCAATGCCAT     1200

TGTTATTTCC TCCAAATAAG TTTTAAATTT TATAATAGTT TTTTTCGTAG CTAGksTACG     1260

CTGTGTAGCT TAAGATTAAG CCGCGTCTTC TTTGCTTTCT GCAACCGCTT TGACTGCAAG     1320

AGCAACGTTG CGCACTGGCG CTTGAAGTAC AGAAAGGAGC ATAGAAAGAA GTCCTTCGCG     1380

GTTTGGAAGA GTTGCAAGTG CAAGAATCTC TTCTTTAGAT GCGACAGCGC CTTCGATTGC     1440

ACCACCTTTA ATTTCAAGTG CTTCAGCGTT TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG     1500

TGCGATAACA TCTTCATTAG AAAATGCTAC TGCAGATGGT CCAACAAATA CAGATGCAAG     1560

ATCTTCAAGA CCAGCTTTTT CAGCTGCACG ACGCAAGATT GAGTTTTTAA TAACTTTATA     1620

CTCAACTTCG CTTCCACGAA GCTCACGACG AAGAACTGTA TCTTGCTCAA CTGTCAAACC     1680

ACGAGCGTCT ACAACGACGA TAGATGCAGC AGCTTTCATT TTTTCAGCTA tACGTCAACT     1740

AGTTCCGCTT TTTTAGCAAT AATTGCTTCA CTCATTAGTG TGTTCACCTC CGTAATTATT     1800

TTGCTTGGGG AATTTTTCAA AAAGAAAAAC GCGCCCAATC CTAGACACGA AAGTACAATA     1860

CGCTTCTTTT TACATGATAC GTTTTGTCCT CGGTAGGATA TTTATGAGTC GAGCTCCCCT     1920

ACTGTCTTAG GCAGTTTTTT TAGATACGG                                      1949
```

(2) INFORMATION FOR SEQ ID NO: 290:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1023 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```
GGACTGTTTG ATCTTATACA GTAGCTGCTT GATCCAAGCT TTCACCGATA GCGGCTAGGC       60

GCTCGATAAC TTCAGCTTGT GTCAATTCAT TTTTTGAAAC ATAGCGGTTA CGTGGGTGAA      120

CACGGCACTC GTGTGAGCAT CCACGAAGGT ACTTGTCTTC ATTTTCTTCT GATGTCAAGA      180

TACGACGGTT ACAGAATGGA TTTCCACAGT TGACATAACG TTCACATGGT GTTCCATCAA      240

ACCAGTCTTT CCCTACGATA GTTGGGTTGA CATGGTTGAC ATCAACGGCA ATACGCTCGT      300

CAAAGACGTA CATTTTCCCA TCCCAAAGCT CACCTTGAAC TTCTGGGTCT TTACCGTAAG      360

TTGCGATTCC TCCGTGCAAT TGGCCGACAT CTTTGTAGCC TTCACGGACC ATCCAGCCTG      420

AGAATTTCTC ACAGCGAACG CCACCTGTAC AGTAAACCAC GACACGCTTG TCCATGAATT      480

TTTCCTTGTT ATCACGGACC CATTGTGGTA ACTCACGGAA GTTGCGAATA TCTGGGCGAA      540
```

1319

```
TAGCTCCACG GAAATGTCCT AGGTCGTACT CATAATCGTT ACGTGTGTCA AGGACAACGG          600

TATCTTTATC AAGAAGCGCT TCTTTGAACT CTTTTGGAGA CAAGTAAGCA CCTGTTGTTT          660

CAAGTGGGTT GATGTCATTG TCAAAGTCGT TGTCTTCCAA ACCAAGGTGG ACAATTTCTT          720

TCTTGTAGCG AACAAACATC TTCTTGAAGG CTTGTTCATT TTCTTCGTCA ATCTTGAACC          780

AGAGTTCTTC CATTCCTGGA AGGCTGTGAA CGTAgTCCAT GTATTTTTGA GTTGTTTCAT          840

AGTCACCTGA AACTGTTCCG TTAATTCCCT CGTCAGCGAC TAGGATACGG CCTTTAAGGn          900

CGATTGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAATTG CTCTGCATTT TCAATTGGAG          960

TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTTGkCaw AAGATTTGTA TCTCTTTATC         1020

TAT                                                                      1023
```

(2) INFORMATION FOR SEQ ID NO: 291:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3831 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```
ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTTCTTAA GAATTTTAAT AGTTTAAAGC           60

ACCTAGCACC TGTTTAGATT GACGAAACAG GATTCGATAC TTATTTTTAT CGAGAATATG          120

GTCGCTCATT AAAAGGTCAA TTAATAAGAG GCAAAGTATC TGGAAGAAGA TATCAGAGGA          180

TTTCTTTGGT TGCAGGTCTA ACAAATGGTG AATTAATCGC TCCAATGACT TACGAAGAGA          240

CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAATTT TCTCTTACCA ACATTAAACA          300

CACCATCGGT TATTATTATG GATAATGTAA GATTCCATAG AATGGGGAAG CTAGAACTTT          360

TATGCGAAGA GTTTGGGCAT AAACTTTTAC CTCTTCCTCC CTACTCGCCT GAGTACAATC          420

CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGGTATTA CCAAGTTGCA          480

ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTTGTTTCAA TTGACTATAT TAGAGGCGAG          540

ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTTGAAGAA AGCGAAGATC TAGAAAGGAC          600

AAATTTCGTC CTTTCTTTTT TGAAGTTTTC AAAGTTCCTA AAACCAAAGG CATTGTGCTT         · 660

GATAAGTTTG ATGAGATTAT TGGTGGCTTC CAGTTTGGCG TTGGAATAAG GTAATTGAAG          720

GGCGTTGACG ATTTTCTCTT TATCTTTGAG GAAGGTTTTA AACAAAGTCT GAAACAGAGG          780

TGGAAAAGCA AGAGCTGATA·GAGATTATAG TGGTGTTTAA AGTCTTCGGA ATAGCTCAAA          840
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                                  1320
AGTTTATCTA GAATTTCTTT ATTAGTCAAG TGCATACGAA AAGTAGGGCG ATAAAATCGT      900

TTATCACTCA GTTTCTGACT ATCTTGTTGA ATGAGCTTCC AGTAGCGCTT GATAGCCTTG      960

TATTCATGGG ATTTCGGATG ATGGCTTGTG TTCTGCTCTC AAGAACAGTT ATGATATTGA     1020

GTTTATCAAA GTCCTGAGCA ATAAAGCTCA TCTCCATCTC CCGATTGAAA CAGTCACTCC     1080

CCGGACTGTT TCAACsTCCT AGGACATAAT CTCAGGAAGA CGCGAAAAAT CATGCTCAAA     1140

GTGAAAATCA TTGTTCTTGC GAATGACAGT TGAAGTTGAA ATAGACAACT GATGATCAAT     1200

GTCGGTCATA GAAGTCTTTT TAATTAGCTT CTGAGCAATC TTTTGGTTGA TGATACAAGG     1260

AATTTGATGA TTCTTCTTGA CGATAGAAGT CTCAGCGAGC TCCATTTTTG AGCAATGATA     1320

GCACTTAAAA CGGCCTTTTC TAAGAAGAAT TCTAGTTTGA ATTTTTTTAT ACTAGAAAAT     1380

CAGAACCATA ATACCTATAT AAAAATATTA TAGTTCTAAT AGGATTTACC CAAAAGTTTT     1440

AAGGCGGTCT TTTTAGAACT TTAATTGTTT GAAATTTAGG TAGCAAATTT GTTTCTATTT     1500

TGTCAACTTT TCCTATTTTT ATCTTGTTGA GGCTGGTATT TTAACAATTC AGGAATTGAT     1560

AGTGAATGTG TAAAATTTTT TGTTAGAATA AGTTTATAAA AAAGAAAAGG AGTATTTGAT     1620

TATGTTACAA AAAATTTATG AGCAGATGGC TAATTTCTAT GATAGTATTG AAGAAGAGTA     1680

TGGTCCTACA TTTGGTGATA ATTTTGACTG GGAACATGTT CATTTTAAAT TTTTAATTTA     1740

TTATTTAGTG AGATATGGCA TTGGTTGTCG TAAGGATTTT ATTGTTTACC ATTATCGTGT     1800

TGCTTATCGT TTGTATCTTG AAAAATTGGT AATGAATCGG GGTTTTATTT CTTGTTGAGG     1860

TAATTTTAGT AAATTTCCGA ACTAATTTAC TCTTTTATGG AAAGATGATA GTAAATAGCT     1920

AGTAATTTTT CTAAATCATT TTTTAATAGT TGGAAATAGC AAATCTTTCT ATTGTTTCTT     1980

CTTGATAAAA AGGCGATTTT TTATTATAAT AAATTGTAAG ATATAATTGC AGGTGAGAGT     2040

CCTGCCATGT ATGTGAGAAA GGAAGAGCCT GATGGCTCAG ACAAGATTAT GACTTCAGTT     2100

GTTGTTGTAG GTACCCAATG GGGTGATGAA GGTAAAGGGA AGATTACAGA CTTCCTTTCA     2160

GCGAATGCAG AAGTGATTGC ACGTTACCAA GGTGGTGATA ATGCTGGTCA CACGATTGTG     2220

ATTGACGGTA AGAAATTTAA GTTGCACTTG ATTCCATCTG GGATTTTCTT CCCTGAAAAA     2280

ATATCTGTCA TTGGGAATGG TATGGTTGTA AATCCTAAAT CTCTTGTAAA AGAGTTGAGC     2340

TATCTTCATG AGGAAGGTGT AACAACTGAT AACTTGCGTA TTTCTGATCG TGCGCATGTT     2400

ATTTTGCCTT ATCATATCGA GTTGGATCGC TTGCAAGAAG AAGCTAAGGG CGACAATAAG     2460

ATTGGTACGA CAATTAAGGG AATTGGTCCA GCTTATATGG ACAAGGCTGC TCGTGTTGGA     2520

ATTCGTATTG CAGATCTTTT AGATAAAGAT ATTTTCCGTG AGCGTTTAGA ACGTAACCTT     2580

GCTGAAAAGA ATCGTCTTTT TGAAAAATTG TATGACAGTA AAGCGATTGT TTTCGATGAT     2640
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1321

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ATTTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT      2700

GTTATCTTGA ATGATGCGCT TGATAATGGC AAACGTGTGC TTTTTGAAGG TGCACAAGGT      2760

GTTATGCTAG ATATCGACCA AGGTACTTAT CCATTTGTTA CGTCATCAAA CCCTGTAGCT      2820

GGTGGTGTGA CAATTGGTTC TGGTGTCGGT CCAAGCAAGA TTGACAAGGT TGTAGGTGTA      2880

TGTAAAGCTT ATACGAGTCG TGTAGGAGAT GGTCCTTTCC CAACTGAGTT GTTTGATGAA      2940

GTGGGAGAAC GTATCCGTGA AGTGGGTCAT GAATATGGTA CAACAACTGG TCGTCCACGT      3000

CGTGTAGGTT GGTTTGACTC AGTTGTGATG CGTCATAGCC GTCGTGTTTC TGGTATTACT      3060

AACCTTTCTT TGAACTCTAT TGATGTTTTG AGCGGTTTGG ATACTGTGAA AATCTGTGTG      3120

GCCTATGATC TTGACGGTCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA      3180

CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTTGGTCAG AAGATATTAC CGGAGTTCGC      3240

AATTTGGAAG ATCTTCCTGA GAATGCGCGT AACTATGTTC GTCGTGTGAG TGAATTGGTT      3300

GGCGTTCGTA TTTCTACTTT CTCAGTAGGT CCTGGTCGTG AACAAACAAA TATTTTAGAA      3360

AGTGTTTGGT CCTAAGAGAT TTTTAAGATT TGTTTAAGAT AGGTCGGGTA TACTATAGAC      3420

GGTTACAAGA AGACCTCCTA ACTTGTTGTA ACAAATATCC TAAACTTTTC TTTTTCATAA      3480

TAATCTCCCT ATAGAGTCAC CGCATTCGGT GGCTTTTTTT GTGTTGGGAT TCATGATATA      3540

ATAATAAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG      3600

AAGTCTTTAT GAGGGAGGCT TTGAGAGAGG CTGAGATTGC TCTTGAACAC GATGAAATTC      3660

CAATTGGTTG TGTGATTGTC AAAGATGGGG AAATCATTGG TCGTGGGCAT AATGCGCGTG      3720

AGGAATTACA GCGAGCGGTT ATGCATGCGG AAATTATGGC TATAGAGGAT GCGAACTTGA      3780

GTGAGGAGAG TGCGCTTGCT GGATTGCACA CTTTTTGTGA CCATTGAACC G              3831
```

(2) INFORMATION FOR SEQ ID NO: 292:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1441 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```
CCGCTGTTCC AACCGCAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCCG        60

TGAAAAGGCG GATGACTTAA CCCCTTGACC AACGGACCTG AGTTGTTATT TTCAACTCTT       120

ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTTT CTAATTTTTG TTTATTTTTT       180
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1322

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CAACTTATAG TAAAAAAAGC CAGAATTATA CTGACTCTTC TATCGCTCAT TAAACTTAGA      240

AGCACGTTCT TTTCCCCACC AATAAGGGAT TAGTTCTGCG ACTTTAACTG TTTTTCTTAT      300

ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC      360

TCTACAAGCA CCGCAAGGCA TGGCTGAACT TCCACCATAA GGTGGTTTGT CTCGAAAGGC      420

TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATTGGTAC ATATTGAAGA GGGCCGCCCG      480

TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAATCCTG TAAATATTTG      540

TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC      600

ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTT TCCCAGATGT CCATTATTGT      660

ATCCTCTTTA TTTAGAGATT TCTTTTAGCA TGTTTTCGAT ATGCTGAATT GATTTTTCAC      720

GTCCAAGCAA GAAAATTGTA TCTGGTAATT CTGGCCCATG CATTTCGCCT GAAACTGCGA      780

TACGAATAGG CATGAAAAGA TTTTTCCCTT TAATACCTGT TTCTTTTTGG ACTGCTTTAA      840

TTTGTGGGAA GATATTTTCT GTCACAAATT CATCATCTGT CATCGCTTCA AGTTTTGCTT      900

TGAATGCTTC AAGAACTGTT GGAACTGTTT CACCCGTCAT GACTTCGCGC TCTGCTTCTG      960

TCAATTCTGG GAAATCTGAG AAGAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT      1020

TCATTTGTGG TTTATAGAGC TCAACTAATT TTTCAGCCTT GTCAGTCAAA CGGCCTGCTT      1080

CCTCTAAGAA TGGTTTTGCC ATTTCAAAGA TGGTTTCAAG GTCTGCATTC TTGATATAAT      1140

CATTGCTCAT CCAGTCTAGT TTTTTCTGAT CAAAGGCTGC TGGTGACTTG CTGAGGCGGT      1200

TTTCATCAAA AAGTTTAATG AATTCTTCAC GAGAGAAAAT CTCATCCCCA CCACCTGGGT      1260

TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTTCTGG AAGGTAACCT TTCTTTCGGT      1320

AATCTTCGAT AAATTGAAGT GTATTAGTAT CACGTTTAGA TAACTTCTTA CCAGTTTCAG      1380

AGTTGATAAT CAAGTGTCAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGAGCGGGTA      1440

T                                                                     1441
```

(2) INFORMATION FOR SEQ ID NO: 293:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4398 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```
CGGCTTATGT AGTGGCAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA GAGGCGCTAG       60

AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAAATGA TGAAGTAGAA GCTGTAAAAA      120
```

1323

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTCG   180

ATTTATCTCT CAACTCTTTT GCCGATATTG AAAATAATCT CTTTGAAGCA GAAGGCTATA   240

ACCATTCATT TCGTTTTCTC AAGGCCAGTC ATCAAATTGA CCAAATTGAG AGTCAAATTA   300

CTTTGATTGA AGAAGATATT GCGGCAATTC GCAATGCTTT GGCAGACTTA GAGAAGCAAG   360

AATCTAAAAA TAGTGGTCGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTTCAGCATA   420

GAGTTGCTGA AAAATTCAGAA CAGTATGGTC AAGCCTTGGA TGAAATTGAA AAACAATTAG   480

AAAATATCCA ATCTGAATTT TCACAATTTG TAACCTTGAA TTCATCGGGT GACCCTGTGG   540

AAGCCGCAGT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAAGT CATATTGTGG   600

ATCGTGTTCC AGCCTTGGTT ACGACGCTTT CTACAGAATT GCCAGATCAA TTACAGGATT   660

TGGAAGCCGG TTATCGTAAA CTAATTGATG CTAATTATCA TTTTGTTGAA ACGGATATTG   720

AAGCGCGTTT CCACTTGCTT TATGAAGCAT TCAAGAAAAA CCAAGAGAAT ATTCGTCAGT   780

TGGAATTGGA TAATGCCGAA TATGAGAATG GACAGGCACA AGAGGAAATC AATGCCTTGT   840

ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAAATCTA CTTGCAACTC   900

TTCCAACTTA TCTTCAACAT ATGAAAGAGA ATAATACTTT ATTGGGAGAA GATATTGCAC   960

GTTTGAACAA GACCTATTTA CTTCCTGAGA CAGCTGCAAG CCATGTTCGT CGTATTCAGA   1020

CAGAATTAGA GAGTTTTGAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAA   1080

CCCAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACTCAA CTAAAAGATA   1140

TTGAAGATGA GCAAATTTCA GTTAGTGAGC GCCTGACACA AATTGAGAAA GATGATATTA   1200

ATGCACGTCA AAAGGCCAAT GTTTATGTCA ATCGTCTCCA TACTATCAAG CGATACATGG   1260

AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGAA GTTATTCTTT ACGGCAAGCA   1320

ATAATACCGA GGATTTAATG GTTGAGTTAG AACAAAAAAT GATTAACATT GAATCTGTTA   1380

CCCGAGTTCT TGAAATTGCA ACGAATGATA TGGAAGCTTT AGAAACGGAA ACTTATAATA   1440

TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACCGC TATCGCTCAT   1500

TTGATGAACG CATTCAAGAA GCATTTAACG AaGCTTTAGA TATTTTTGAA AAAGAATTTG   1560

ATTATCACGC TTCATTTGAC AAGATTTCTC AAGCATTGGA AGTGGCAGAG CCTGGTGTAA   1620

CCAATCGCTT TGTTACCTCA TATGAGAAAA CACGTGAAAC GATTCGTTTT TAATAAAAGA   1680

AAAAGATTTT ATTGTGTGAG GAGCAGAATC AAATCTTTTT CTATAGTTGT GGGGAGATTT   1740

ACTTCATTTT CTCCTGAGAT TGAGTTTTTG CCCAGCCGAT TTATCCACTA CCTCAAAACA   1800

GTGTTTTATA CTCTTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCCTTA CCGTACTCAA   1860

1324

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GTACAGCCTG AGGCTAGCTT CTTAGTTTGC TTTTTGATTT TCATTTAGTA TTAAAGTGAT      1920

TTCGCCAGTC TTATCTGCAG CTTCAAATCT GTACTTTGAG TAACTTGGTA ACCGTCCAAT      1980

AACGAAGTCT ATTGAAAAAT CTCCAGACTA GAGAACTCAC GGATAGTTCC TAATCTGGAG      2040

ATTTCTTATT TGCACTTTTC TTGTACAACT TTAGTCCACG GTAAATAGAC CTCTAAAACC      2100

TCTTTGTTTA CGAGAGTTTC CTCGTTTGGA AGACATTCTA GAAGATAGGA TAGATATTTC      2160

TCGCTATTTA TACTAGACTA AAATCAAAAA GCATTATATA ATAGTGATAT GAAATCAACT      2220

AAAGAAGAAA TCCAAACCAT CAAAACACTT TTAAAAGACT CTCGTACAGC TAAATATCAT      2280

AAACGCCTTC AAATCGTTCT ATAGTAAAAT GAAATAAGAA CAGTACAAAT CGATCAGGAC      2340

AGTCAAATTG ATTTCTAACA ATGTTTTAGA AGTAGAGGTG TACTATTCTA GTTTCAATCT      2400

ATTATATTTC GTCTGATGGG CAAATCTTAT AAAGAGATTA TAGAACTTTT ATAGTAGATT      2460

GAAATAAGAT GTGAACAACT CTATCAGGAA AGTCAAATTA ATTTATAGAA ATATTTTAGC      2520

AGCCAAGGTG TACTGTTATA GATTCAATAC ACTATAGACT GTAATCAAAC AACGATTTGG      2580

CGAAATGTAA AAAAATATGA GGAGTTCGGA CTCGACTCTC TCCTTCAAGA AACACGTGGT      2640

GGTCGTAACC ATGCATATAT GACAGTTGAG GAAAAGAAAG TCTTTCTTGC CCGCCATTTG      2700

AAGGCTGCAG AGGCAGGAGA ATTTGTTACA ATTGATGCCT TATTTCAGGC TTATAAAAAG      2760

GAGTTAGGTC GTTCCTACAC ACGTGATGCC TTCTATCAAC TGTTGAAGTG CCATGGTTGG      2820

CGAAATATTA TGCCACGTCC AGAACATCCT AAGAAAGCAG ACGCTCAAAC CATTGTCGCG      2880

TCTAAAAATA AAATCTCAAT TCAAGAAGAA AAGAAAGCGC TTTAAAACCA GTAGACGTTT      2940

TCGTAAGGTT CGCTTGATGT ACCAAGATGA GGCTGGTTTC GGTAGAATCA GTAAACTGGG      3000

ATCTTGTTGG GCTCCAATAG GAGTAGGTCC ACATATCCAT AGTCACTATA TACGAGAATT      3060

TCGCTATTGT TATGGAGCTG TTGATGCCCA TACAGGCGAA TCATTTTTCT TAATAGCTGG      3120

TAGATGTAAT ACTGAGTGGA TGAACGCCTT TTTAGAAGAG CTTTCACAAG CTTATCCAGA      3180

TGATTATCTT TTACTCGTTA TGGACAATGC TATATGGCAT AAATCAAGTA CCTTAAAGAT      3240

TCCGACTAAT ATTGGTTTTA CCTTTATTCC TCCATACACA CCAGAGATGA ACCCCATTGA      3300

ACAAGTGTGG AAAGAGATTC GTAAACGTGG ATTTAAGAAT AAAGCCTTTC AAACTTTGGA      3360

AGATGTCATG AATCAACTCC AAGATGTTAT ACAAGGATTG GAGAAGGAGG TGATAAAGTC      3420

CATCGTTAAT CGGAGATGGA CTAGAATGCT TTTTGAAAAC AGATGAGTAT AAAAAGAAAG      3480

TCCTCATTTC AATAGAAATC ACGACTTTCT GATGGATTTA TAGTAAAATG AAATAAGAAC      3540

AGGACAAATC GATCAGGACA GTCAAATCGA TTTCTAACAA TGTTTTAGAA GCAGAGGTGT      3600

ACTATTCTAG TTTCAATCTA CTATATTTTT GGAGTGATAG AAAAGCCCTT CATAAGCTAG      3660
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1325

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TCTACTTGTT CAGGTGCGAG AGCTTTGACA TCTTTTTCTG TACTTAGCCA AGTCAGTTTT    3720
CCGTTCTCAA AGCGTTTATA TAGTAGCCAA AATCCTTGAC CATCCCAGTA AAGGGCTTTA    3780
AAGCGGTCTT TACGTCCACC ACAAAAGAGA AAGACTTGAC CGGAGAAAGA ATCCAATTCA    3840
AAGTGGGTTT TAACTACATA GGCTAATGAG TCTATTCCCT GCCTCATATC TGTCTTGCCA    3900
CAAACAAGGT GAACTTGACC TAAATCACTT AGTTGAATTA TCATAGTACA ATACCTTTCC    3960
TCCGATAATT ATTTTTTATC TAGTATACTG GAAGTTGGGG AATTAGGATA GATACCTTGT    4020
TATGACGCGC TTACGTAACT TGTAACTAGC TGCCTAGTTT GATCTTTGCT TCTTCATTGA    4080
TTAGCAGTAG ATTTCAAAAT GATAAAAACG CATAGTATCA GGTATTGAAA TGTACTGCCC    4140
CAAAAGTTAG ACAGAAAAAA TCTAACTTTT GGGGTGTTTT TGTTATGAAA TTAAGTTATG    4200
ATGATAAAGT TCAGATCTAT GAACTTAGAA AACAAGGATA TAGCTTAGAG AAGCTTTCAA    4260
ATAAATTTGG GATAAATAAT TCTAATCTTA GGTATATGAT TAAATTGATT GATCGTTACG    4320
GAATAGAGTT CGTCAAAAAA GGAAAAAATC GTTACTATTT TCCTGATTTA AAACAAGAAA    4380
TGATTAATAA AGTCTTAC                                                  4398
```

(2) INFORMATION FOR SEQ ID NO: 294:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 718 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```
AGATTTTTAG ACTTTGTCTT TAATCGTTTC TTTTTAGGGA TGATTGCGAC ACCTTCTTTT     60
GGCTATTAAC TTTAGCAGGA GGGATTATCC TTGGTCTAGC GCCGGCTAGT GCCACCTTGA    120
TGAGCTTATA TGCAGAACAT GGTTATAGCT TTCGGGAATA CAGTTTGAAG GAGGCTTGGT    180
CTCTTTACAA GCAAAATTTT GTCTCAAGCA ACCTGATTTT CTATAGCTTT TTAGGTGTGG    240
GTCTAGTTTT GACCTATGGT TTGTATCTCT TGGTGCAATT GCCTCATCAG ACCATTGTTC    300
ATTTGATTGC GACCCTTTTG AATGTCCTAG TAGTTGCCCT GATCTTTTTG GCTTATACAG    360
TATCTTTAAA ATTACAAGTT TATTTTGCCT TGTCCTATCG AAATAGTCTC AAATTATCCT    420
TGATTGGCAT CTTTATGAGT CTAGCAGCTG TGGCTAAGGT TCTCCTTGGG ACTGTGCTAC    480
TTGTAGCAAT TGGTTATTAT ATGCCTGCCC TGCTATTTTT TGTAGGAATT GGGATGTGGC    540
ATTTCTTTAT CAGTGATATG TTGGAACCTG TCTATGAAAT CATCCATGAA AAATTGGCGT    600
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1326

CAAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGATG   660

ATCATTATCA TTGCGAGTTT TGCAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTG   718

(2) INFORMATION FOR SEQ ID NO: 295:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 718 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCTGGAT TTATACTAGC AAAGATCCAA GAGCAAATTA TTTAACAGAT   60

TTAGGTCTAG TTTTCCCTGA ATCATTAAAA GAATTTGAGA GTGAAGATAG TTTTGCAAAG   120

GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT   180

GATGATAAAA CTCTTGAAGC TTTACAAAAA GATCCTCTTT TAGGTAAAAT AAATGCAATT   240

AAAAATGGTG CCGTTGCTGT AATTCCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA   300

ACACCACTTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC   360

AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAATT TTTATAATCT GCCTAGGTCT   420

TCTTATTACA ATATTTTTGT CATTAAAGCT TGGAACAAAA GAAATTAATA TCAGAGATTT   480

TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAAATCAA TTATATATAA   540

rAGAATACCT AGAACTATTT TTGCAATTTT AGCAGGTTCT AGTCTTGCCA TAAGCGGTGT   600

ATTGATGCAA TCAGTTACTA GAAACCCAAT AGCTGATCCA GGTATACTCG GTATAAACAC   660

AGGAGCAAGT CTTAGTGTAG TAATTGGTCC TTCtTTTTAG GGAATTCATC AAGCATAA   718

(2) INFORMATION FOR SEQ ID NO: 296:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1436 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAACTAATCA TTTTTACAGG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAGG   60

TTTTTCTTGG CATAATGACT TTTCCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA   120

CCAAGTCCAC sCTTAAGTTA GATAATAAAT CTAACTTAAG GAAGCTAGAA GGATGAGAAT   180

CCAGGTGGTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAATAA TTTGCTTTTT   240

1327

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GAAGGCAAGG CCACGTTCCT CTATATTGGG AAGTGAGAGT TGAATGAGAG AACCAGCTGA        300

TGAAAAGGGT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG        360

AATATCAATC TGAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC        420

TACAACGGAT AGGGTGGAAC TAAAGAGTGA CATCACTCCG GCTATCACAC AAAAGAACAG        480

AGGTAACCAG AAATGAGGAA TGGTTGTTGT CATGAGGTGC CCTATCAGTG TGACTAAACC        540

TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGCAG AGCATGATAA TTGTAGCCCA        600

GGGAACCTTA GCTAAAATGG CTTCTTGCTT CCCTAATTTG AGCCTTAAGG CGAGGCAGAC        660

CATGAGTATT GAGACAAAGC CAATATCAAA TGTTTTTTGA TAAGTAGCTA TCCAGGCGAT        720

GTTTGGGAAA ATGAGATGCA ACAAGGGAAA AAGCCAAACC AAAACCATGC TGCTGATCAT        780

GAGCAAGGTG GTTTGTCTTT GAACCTTGCT GAGGAGTGGT GGTTGGTCAA TAGTCAAGGA        840

TGAGTTTGTT CTTCCCTTAC TATAGTGACT GTAACAGGAT AATAAAAGCA AGACGATGAG        900

TGGGTAGATA ATGCTGACGA TAAAGATATG ATTGCCAAGT GAAAAAGCTT GCTCTTCCCA        960

TCCCATTTGC TTAAACAGGC CTTGAAAGAC AATGCCTGAG CTACTGGTTA TCAAATTAGC       1020

CCCTCCTGAA GCTCCCCAAT TGACGGCTTG AGCTCCAATC AAAGGGTGTT TGTCCGCTTT       1080

TTGACAGAGG GTAATCGCTA GAGGACAGCA AACGGCCATA GTAGTGAAAA ATCCAGCACC       1140

TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAAATCATG TAGAGGGCGT TAGGGTGGGT       1200

GCGTGTGCGG TAGAGAATGT GTTGAGCCAA AACATCAAGA GTACCGTTAG TTGTTGCAAC       1260

GTTATAAAAG AGAGAGACGC TAAAAATGGT AAAAAAGAGT GAGGTTGGCC AAAAATGAAG       1320

AAGTTCTTTG GGGCTTAATC CCATGAGAGT GGTTGCGATG AGGTAAGAAA AAGCAATAGC       1380

CAGCAGGCCA ATATTGATTT TGGTGCGGTA ACCAATTCCA ATGGCTAGAG CAATGG          1436
```

(2) INFORMATION FOR SEQ ID NO: 297:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1696 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```
CCATTTGGGA AAGAACGTAA GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA         60

GCCGTTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAATGG TGTGGACAGT        120

CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACGTAT CAACAGTAAC CAACTGCTAC        180
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1328

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AAGGCGGCTG TGGATGCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC     240

TTGGTGGACG AGATGTGGAA GGTTGCCCAA CGTGAACTGG CTACAGGATT TTACTATGGT     300

ACACCATCTG AAAATGAGCA GTTGTTTGGT GCTCGCCGTA AAATTCCTGA GTACAAGTTT     360

GTCGCTGAAG TGGTTTCTTA TGATGATGCG GCACAAACAG CAACAATTCG TCAACGAAAT     420

GTCATTAACG AAGGGGACCA AGTTGAGTTT TATGGTCCAG GTTTCCGTCA TTTTGAAACC     480

TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATCG ACCGCGCTCC AAATCCAATG     540

GAACTATTGA CTATTAAGGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCATTA     600

AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA     660

GAAAGGAAAA GGAAATGATA GAGGCACAGG GTTTCTTAGT GGATAAGCAA ACAAGATGCA     720

TTCATTACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATTGT AAAAAGTATT     780

ATGCTTGTTA TCGGTGTCAT GATTCATTAG AACATCACCC TTTTGAGCCG TATCCCTTAT     840

CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAAACTACTA ACATATAAGC     900

AATATAAAGA AAGCTTAAGT TGCCCCTTTT GTTTTTCTCG CTTTAATCCA GGTTGCCAAA     960

ATCATAAGGA ACGCTATTTT AAATAGCAAA TCATCTAGTT TTGAAGTAGG AGAAAACTCA    1020

ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAAC GCATAATATC AAGATTGTTC    1080

AATACCTGAT ACTATGCGTT TTTAAGATTT TAAAGACTTT TTTCCTTTAT CTGGTATTTT    1140

GACTACTTGT TAAAACTGGG TTAATTTTCG ACTGTTTAAT AGTTATTATG CAAAGTCTAA    1200

AAGGTTAGAA TTGTCAAAAC AATCCGTCTA GAGTATGCGT GATGCCAACC GTGGTGGATG    1260

TTCTCAGTCA TGCCGTTGGA AGTACGACCT TTACGATATG CCATTTGGGA AAGAACGTAA    1320

GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT    1380

TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAAAAATCG AAGGACGTAT    1440

GGAGTCTATT CACTATGTAT CAACAGTAAC CAACTGCTAC AAGGCGGCTG TGGATGCCTA    1500

TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC TTGGTGGACG AGATGTGGAA    1560

GGTTGCCCAA CGTGAACTGG CTACAGGATT TTACTATGGT ACACCATCTG AAAATGAGCA    1620

GTTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTTT GTCGCTGAAG TGGTTTCTTA    1680

TGATGATGCG GCGGTA                                                   1696
```

(2) INFORMATION FOR SEQ ID NO: 298:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1022 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```
CCGAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTTGCT TGCAATAAGA     60
AAGAAAGTCT TTATAGTCAA AGCAAATTTA AGTATGCGAT TCGTTCGATG TTCGCAGGTG    120
CATTTTTAAC CTTCAGTACT GCTGCAGGTG CAGTTGGGGC TGACTTGATT AATAAAATTG    180
CACCAGGTAG TGGACGCTTC CTCTTTCCAT TCGTTTTTGC TTGGGGCTTG GCCTACATTG    240
TTTTTTTGAA TGCCGAGTTG GTCACTTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT    300
TAAAAAAAAT CTCTTGGAGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTCAACC    360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT GCGAATCTGA    420
CACACGATAG TTTCATCTCA GGTGTTGTTG AGATGAAGTT AGGCCGCTCA AATGAATTGG    480
TCTTGCTTGA GGCGATTTTG GCAAATATTT TTGTAAATAT TGCGATTCTG TCATTTATTT    540
TGGTCAAAGA TGGTGGTGCC AAACTTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT    600
TCTTAACAAA CGAGCACATT GCGGCGAACT TTGCTTCTTT CGCCGATTGTG AAATTCAGTG    660
TTGCTGCGGA TTCAATTGCC AACTTCGGTG TTGGAAATAT GCTTCGCCAC TGGGGTGTGA    720
CTTTCATCGG AAACTTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA    780
ATAAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTTTT    840
CATTTTCAAA ATAAGGTAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTTGT    900
ArACTATAAC TCAAGGTGCT ACAATATCCT TAATAAAATA ATATGGAGGT CACCTTATGA    960
CTTGTGATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA   1020
CT                                                                 1022
```

(2) INFORMATION FOR SEQ ID NO: 299:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 663 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```
CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GGGAATATCG ATATAATGGC     60
TTCATTATGA GTGGCAGGAA TATCCAATAT GGCAACTTTT CCAATAGATA ATTTAAAACT    120
CATTAATAAA GTTCCTTTAG GTGAAATGTC TATTTTCTTT GATTTTAATG CTAATTTAGA    180
```

```
                                     1330
AATAGATTCT CTCGCATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA    240

AGGTATTTCA GTTCCCCAAA AAGTAGCTTC ACTGCGTGGA GGAGTTTTTC CTATTCTGAA    300

GTTAACTAGG CTAGCAAATT TAATATATCT CCATGCTTCT GGGATTTCAT ATATAGGATA    360

AGAGGTTGTT TCGTCTTTGT TCCCATAATA AGAGTTATCA TCTCCTTGGG AAACAATAGA    420

AATGTCCAAA TCTTTCTTTT TAATCTTGCC TTCTTCAAAG AGTTTTTGTT TTTCTGCTCG    480

TATTTTTTCA AGTAAAACTT CGACTGATTC ATCATTTGGG TCTTGTTCAA CTAATTTTCC    540

TTGCATAGCA TATTGAAGAA TAGATTTTTT TAGTTTATCT GGAAATTCTT TATCTAGCTG    600

TTCTAGTCTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC    660

TTC                                                                 663
```

(2) INFORMATION FOR SEQ ID NO: 300:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 881 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```
CGTCGCTGAA CATGTCAACA GCAAATTAAA CTAAACAAAC TAAAATTATG TGATACTTCA     60

CATAATTTTC TTTAGAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAAACAT    120

ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAAGAA TTGAAATTGG    180

TTCGTCGACC AGAAGTGGTA GAACGCATTA AGATTGCCCG TTCATACGGT GACCTTTCAG    240

AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAAGCCTT TGTCGAAGGA CAAATCTCTA    300

GCTTAGAAAC AAAAATCCGC TATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG    360

AAGTAGCGAT TGGTAAAACA GTCACCATCC AAGAAATTGG TGAGGACGAA GAAGAAGTTT    420

ATATTATCGT AGGTTCAGCT GGTGCAGATG CCTTTGTAGG TAAGGTTTCA AATGAAAGCC    480

CAATTGGGCA GGCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCCTG    540

TTGGTAGCTA TGATGTAAAA ATCTTGAAGG TTGAAAAAAC AGCCTAAAAA CAGAAAAAGG    600

AGTGGGGAGG CGATGTGCTT CACTCACTCC TTTTTCCATT TTGCTACTCT TCGAAAATCT    660

CTTCAAACCA CGTCAGCGTC GCCTTGCCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT    720

CTACAACCTC AAAACAGTGT TTTGAGCTAA CTTCGTCAGT TTCATCTACA ACCTCAAAAC    780

TATGTTTTGA GCTGACTTCG TCAGTTTCAT CTACAACCTC AAAACCATGT TTTGAGCCGA    840

CTTCGTCAGT TTCATCTACA ACCTCAAAAC TATGTTTTGA G                       881
```

1331

(2) INFORMATION FOR SEQ ID NO: 301:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 949 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```
CCTTTTTTAA TACAAGTTAT TTTGATTTAA CCGGCTTGTC TTGAGCTGTC TGCAAAGCTG        60

TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTCGAT AGTGCTACTC TCACTCCCGA       120

AATGAACCTG GTCTGTTCCA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT       180

CTGCTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCTCT CATATAGGCA GCAGCCTTCT       240

CAACGATGGC ATAGGTCTCT TTTGTCTTAT CTCCCTCATA AGGAGTCACC AAAATCATAT       300

GGTGTCCCTT AGGAAGATTT TTCACGATAC TGTCCCAGTC ATCCTTGTAA TTCTCAGGAT       360

TATTTACCCC AGTCGCAATG ACCACCGTCT TAGGTAAAAA TTTATTCTGG CTATTATTTA       420

GCATGATTTC ATTTGCGGTC TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG       480

GAAGAGCTGT CTGTAGTGCT GTATTTGCCC TTAAAGCCAC TGAGTCACCA ATTAACATAG       540

TGCCATCAGC AATTCCCAAA CTGTTTGCAT CTGCCCGTTC TGCCATCACC TTGGTCTGGC       600

CAATATTTGT TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA       660

CTTGTGGTGC CAACAAGGTC ACCGTGCAGA CAATGATGGT CAAGATTCCT GTACCTGCTG       720

CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAsGGTTTG GACAATAGGT GTGTTCTTGC       780

CTGCAATCCA AGGTTCCAAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA       840

GAGTCAGTAA TACAGCAAGA AGATTTGATG TCAACTGTGA GAAAATGATA TAGAAAGGCC       900

AATGGAAAAG ATAAACCGCA TAGCTAGTAT CCGCTAAAAA GCTGATAAT                   949
```

(2) INFORMATION FOR SEQ ID NO: 302:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 622 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```
AAGATATATT TTTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT GGAATTAAAG        60
```

1332

CGAAAATAAA AGCCGTGTAC AGGCGACCAA ACCAACGTAC ACGGCTAAGG AAAAATAACA   120

AAACTCAAGC AAAGGCAAGG CGCGTGGTTT TGTTAGGTAT TTAGCAAGGG GACAAACCCC   180

TTTGTAAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTTATA   240

AAAAGGAAAA ATGGAGGATA TAAATGGAAA TTCTGTCTAA AGAAATACAG TTACAGGGCT   300

TACAACTTCT TAAACAGACT CTTGAAACTT TAGTTGAGCT AGAAAAACAA CGATCTAGTA   360

AGTTAGATTT AATTTCTCGT AAAGAATTAA TGGATCTGCT AGGTATAAGT GCTACAACCC   420

TTGATAACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA   480

AAGTATTCTA TCGTCCGTCA GATGTGTATT TATTTTTAGC AATAAAATAG GAGTTATGAA   540

ATGAAAATTG TTACTTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTA ACTGCCAGGT   600

ATTGACATTC TATTTGTCTC AG   622

(2) INFORMATION FOR SEQ ID NO: 303:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1929 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAACTTG CAAACAAAAG AAGAACGCAA ACTCCACAAA TCCTTTACGC AGAAACTCAA   60

TCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCAGTAA   120

ACGTAATTTC TAAATCAGGT ACAACAACTG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG   180

AACTCTTGGT TAAGAAATAC GGTCAAGAAG AAGCTAACAA ACGTATCTAT GCAACAACTG   240

ACCGCCAAAA GGGTGCTGTT AAGGTTGAAG CAGACGCTAA CGGTTGGGGA ACATTTGTTG   300

TTCCAGATGA TATCGGTGGA CGCTTCTCAG TATTGACAGC CGTTGGTTTG CTTTCAATCG   360

CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAGGTGC GAATGCAGCT CGCAAAGACT   420

ACACTTCAGA CAAAATCTCT GAAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC   480

TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAAACTA TGAGCCATCA CTTCAATACT   540

TCTCAGAATG GTGGAAACAA TTGGCTGGTG AATCAGAAGG AAAAGACCAA AAAGGTATCT   600

ACCCAACTTC AGCCAACTTC TCAACTGACT TGCACTCACT TGGTCAATTT ATCCAAGAAG   660

GAACTCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA   720

TTCCTACTTT GGAAGAAGAC CTTGACGGAC TTGGTTACCT TCAAGGAAAA GACGTTGACT   780

TTGTAAACAA AAAAGCAACT GACGGTGTTC TTCTTGCCCA CACAGATGGT GATGTACCAA   840

1333

ACATGTATGT GACTCTTCCA GAGCAAGACG CTTTCACTCT TGGTTACACT ATCTACTTCT   900

TCGAATTGGC AATTGCCCTT TCAGGTTACT TGAATGCTAT CAACCCATTT GACCAACCAG   960

GTGTTGAAGC TTATAAACGT AACATGTTTG CCCTTCTTGG AAAACCAGGA TTTGAAGAAT   1020

TGAGCAAAGA ACTTAACGCA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACTCTTTT   1080

TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA   1140

AAAAGGCAGA CGCCTAGATA ATAGGAGAAA CTATGTCAAA AGATATCCGC GTACGTTACG   1200

CACCAAGTCC AACAGGACTA CTACACATCG GAAATGCTCG TACAGCATTG TTTAATTACT   1260

TGTATGCGCG CCATCATGGT GGAACATTTC TCATCCGTAT CGAAGATACT GACCGTAAAC   1320

GCCATGTCGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT   1380

GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCCAGTC TGAGCGTTTG GACTTGTATC   1440

AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAAGCCTA TAAATCTTAC GTTACAGAAG   1500

AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTGG CGAAACACCA CGCTACATCA   1560

ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG   1620

CAGGGATCAT CCCAACTGTT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATG   1680

ATATGGTCAA AGGCGATATC GAATTTGAAG GTGGCAATAT CGGTGGTGAC TGGGTTATCC   1740

AAAAGAAAGA CGGTTACCCA ACTTACAACT TTGCCGTTGT TATCGATGAC CACGATATGC   1800

AAATCTCTCA TGTTATCCGT GGAGATGACC ATATTGCTAA TACACCAAAA CAGCTTATGG   1860

TCTATGAAGC TCTTGGTTGG GAAGCTCCAG AGTTCGGTCA CATGACCTTG ATTATCCACT   1920

CTGAAACTG   1929

(2) INFORMATION FOR SEQ ID NO: 304:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 708 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTTAAGA AAAAGGAGAC ACATCATGTC TAAAAAAGTA TTATTTATCG TCGGATCACT   60

ACGTCAAGGT TCTTTCAACC ACCAAATGGC GCTCGAAGCT GAGAAAGCAC TTGCTGGTAA   120

AGCGGAAGTT AGCTACCTTG ATTATTCAGC CCTTCCTCTC TTCAGCCAAG ATTTGGAAGT   180

TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG   240

1334

```
GATTTTCTCT CCAGTCTACA ACTTCTCTAT CCCTGGTACA GTGAAAAACT TGCTTGACTG       300

GCTATCTCGT GCCCTTGACT TGTCTGATAC ACGTGGCGTT TCTGCCCTTC AAGACAAGTT       360

TGTCACAGTA TCATCTGTAG CCAATGCAGG GCACGATCAA CTTTTCGCTA TCTACAAAGA       420

CCTCTTGCCA TTTATCCGTA CACAAGGCGT TGGTGATTTC ACTGCTGCAC GTGTTAATGA       480

CTCTGCCTGG GCAsACGGAA AATTGGTTCT TGAAGAAACA GTCCTAAACT CACTTGAAAA       540

ACAAGCTCAA GACTTGGTCG AAGCTATCAA GTAACTAACA CTCAATAAAA ATCAAAAAGC       600

AAACTAkGAA GCTArCCGCA AGCTACTCaA gCACTGCTTT GAGGTTGTAG ATAGAACTGA       660

CGAGTGTnnA ACATATATAC GGTAAGGCGA CACTGACGTG GCTTGAAn                    708
```

(2) INFORMATION FOR SEQ ID NO: 305:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 781 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```
CTTCTTTTCT TGGAAATAGG TGTATAATAC GTTTATTAAA TTTTTGAGGA GTTGTCTATG       60

AAGAAAGTT TTATCCATCA ACAAGAAGAA ATTTCCTTTG TCAAAAACAC TTTTACCCAG        120

TATTTGAAAG ATAAGCTAGA AGTTGTCGAA GTTCAAGGTC CTATCTTGAG TAAGGTCGGT       180

GACGGAATGC AGGACAACCT GTCTGGTGTG GAAAATCCAG TATCGGTCAA GGTTCTCCAA       240

ATCCCTGATG CTACTTATGA AGTGGTGCAC TCACTTGCTA AATGGAAACG CCACACCTTG       300

GCTCGTTTTG GCTTTGGTGA AGGAGAGGGT CTCTTTGTCC ACATGAAAGC CCTTCGTCCA       360

GATGAGGATT CCTTGGATGC AACCCACTCT GTTTATGTTG ACCAGTGGGA CTGGGAGAAG       420

GTTATCCCAA ATGGTAAGCG TAACATCGTT TATCTAAAAG AAACAGTTGA GAAGATTTAT       480

AAGGCTATTC GCCTGACTGA GCTAGCTGTT GAAGCCCGCT ATGACATCGA GTCTATCTiG       540

CCAAAACAAA TTACCTTTAT CCATACAGAA GAATTGGTAG AACGCTACCC AGACTTGACA       600

CCGAAAGAAC GTGAAAATGC GATTTGTAAA GAATTTGGAG CCGTCTTTTT GATTGGTATC       660

GGTGGCGAGT TGCCAGATGG TAAACCGCAC GATGGACGTG CACCAGACTA TGATGACTGG       720

ACAAGCGAGT CTGAGAATGG CTACAAGGGT CTAAATGGTG ATATTCTTGT CTGGAATGAG       780

T                                                                     781
```

(2) INFORMATION FOR SEQ ID NO: 306:

    (i) SEQUENCE CHARACTERISTICS:

1335

(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```
CCCGCATCTT GTAGGGTTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGTTTTAGCC        60

GCTTCTAGGG CTGTTTGGTA GTTGTTTTTC GCGTCCGGAT GCGCCTTTTG TTCTTCTTCG       120

CTAACAGGGT TATCAGGAGC AAAGAAAATA GCAGCACCTG CCCTAGCCGA AGCTACAACC       180

TTCTTATCAA TACCTCCAAT GTCTCCCACA TTACCATCGC GGTCAATGGT ACCTGTACCG       240

GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA       300

AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG       360

CTGATTACCT CTGTACGGTC AATCAAGCCG ATTCCAATTC CATTTTTGCC ATTTTCCAAG       420

GTGATGATTT TTCCTTCTGC AGACTTGGTT TGCCCATCCT CTTCATAGGT GACCTTGACG       480

GAATCCCCTA ATTTTTGAGA ACTGACGTAA TCAATCAAGT CTTTGGAACT ATCAAAGGTC       540

TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTTGAATTA       600

TCCGTCACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT       660

TTTAGTCCTT GATACTTGGC CATATTTTGC GATGTTTGCA TGTAGAATTG ATTGATTCGC       720

ATAAATTCAA CATCGGAAGA ACCACCTGTA GTCTCCTGAG CACTACGAAT ATCTGTAAAA       780

GGTGTCAACC AAGCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACG       840

AATTGT                                                                  846
```

(2) INFORMATION FOR SEQ ID NO: 307:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 829 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```
GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC        60

CATATAAAGT CCACCCCCCA TGGCACCGAC AAGAGCTACA TAAAAGAAGC TCCACAAACG       120

TCCACTTGGT TGGAAGAAAA ATCCTAACAG CCACTGGATG GTTCCTATTA ACAGAAACAT       180

GACTAGGGTC AGCAAACTGA TTAAAATGGT TCGCTTCAAA ATCACCTTGC GCTTGACACC       240
```

1336

```
AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT        300

TGAAATCAAA GGACCATAAC TGTGGAAGAG GGCGATGGTA GGTAGTTGCA AGACTAGCTT        360

GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTTGCGG TTGCGGAACA TGGCCTGAAG        420

CATTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC ·TGCAAAACTG CAAAGACAAA        480

TAAGCCCAGA GCCAAACTAT CTGGCTTACC ATAGAAGACC GTATAAAGAG GTTCTCCTAC        540

CATAACCACT CCAACCGTTG CTGGTAGCAA GAACATAAAG AGTAGGGTGA GACTGTCCTG        600

AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTTGACATAG TTTTCCGTCA AAAGTGGCAA        660

ACCAACACTC CCAATCGAAA CCCCTACAGA AATCAAAATC ATCGTGATTT TATTAGGATT        720

GGCTGAGAAA TAAGAAAACA TGACAACCAA GTCCTCATTG CTGTAGTTGG TAAACCAGCT        780

CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG                .    829
```

(2) INFORMATION FOR SEQ ID NO: 308:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 464 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```
CGAACATCTT GCTGGCTGAT TCGTCTGCCG CCATCGCAGC CCCGAACACA TTGCGACCCA         60

TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCCCCGCGTG TGCATCATTT        120

GCTCATCTAG TAACGTATGA GGTTTGCCTT CGCTGTCGAT AAACCGATAT TCAATCGCAC        180

CACTGCTCGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAACTCC AGAGAAGAGA        240

GATCACGACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTAGCAGC AGGCTCGCCA        300

CCACGCATTC CCAGAACTCA ACGGGGGTTT GATCGGCGTT CGGTTGCTGA CTAATAACTC        360

GGTGCACGGG ATGCGAAGTG GCCACTTCTG GCACACCGTT CTTGTCTTCG TAGAGAGCAA        420

TTGGGAGGGT GGCCAGCGTT TCGGCGATGA GGCGCACGCA GGCC                        464
```

(2) INFORMATION FOR SEQ ID NO: 309:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 982 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

```
CCGTCTATAA TGGTAATAGA TTTTATTTGG AGGTTTTTAT GTCATTTCTA TCAAAAAATG        60

GAGCAGGTAT CTTGGCCTGC CTTCTCATTT CCATCCTATC TTGGTACTTA GGAGGATTCT        120

TCCCTGTGGT TGGCGCGCCC GTTTTTGCCA TTTTCATAGG CATGCTCCTA CATCCCTTTC        180

TCTCGTCCTA TAAACAACTG GATGCTGGTT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT        240

ATGCCGTTGT CTTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGGCCAAT        300

CTTCACTCCC TGTCATCCTG TCCACTATCT CAATAGCTCT GATTATTGCC TACCTCTTCC        360

AGCGTTTCTT TGCCCTGGAT ACAAAACTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT        420

GTGGGGGTTC TGCCATTGCA GCGACAGgCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC        480

CCAAGCCATT TCCGTTATCT TTTTCTTCAA TGTCTTGGCT GCGCTCATCT TTCCAACCCT        540

CGGCACCTGG CTTCATCTAT CCAATGAAGG CTTCGCCCTC TTTGCAGGGA CTGCGGTCAA        600

CGACACTTCC TCTGTAACGG CTGCCGCCAG CGCTTGGGAC AGTCTTTACC AAAGCAATAC        660

CCTCGAGTCT GCAACCATTG TTAAACTCAC ACGTACTTTG GCCATTATCC CTATCACGCT        720

CTTTCTATCC TACTGGCAAA GTCGCCAACA AGAAAACAAG CAAAGCCTGC AACTGAAAAA        780

AGTCTTCCCA CTTTTTATCC TTTACTTTAT CCTTGCCTCT CTCCTCACTA CACTACTCAC        840

CTCTCTAGGT GTGTCCAGTA GTTTCTTTAC TCCTCTCAAA GAACTCTCTA AATTCCTTAT        900

TGTCATGGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTCGCTATGG TCAAATCCAG        960

TGGAAAATCC ATTCATCATG GA                                                982
```

(2) INFORMATION FOR SEQ ID NO: 310:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1939 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```
CTAGCTGCCA ATATGATTGG GGTGCAGAAG CGCGTGATTA TCTTTAATCT TGGCTTGGTT        60

CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA        120

GGCTGTTTGT CCTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGCC        180

TATCGTGACA GCAAGTGGCA GGAACAGACC ATTACCTTGA CAGGCTTCCC AGCTCAGATT        240

TGCCAGCATG AGCTGGATCA CTTGGAAGGA CGAATCATTT AGGAGGAAAG CAAATGAAAC        300

GAATAGTCTT TGAACTTATT TTTATCGCAA CGACCTGGTA TATCTTTTTA CCGCCCCTTA        360
```

1338

```
ACCTGACCAG CTGGGAATTT CTCTTCTTCC TCTGTGGGCA TTTGTTAGTT GTGGCAATAT     420

TATTTGGCTT TGGCAAGGGG ATAAACCTTG TCAAAACGGT TCATGTGCGC CACGGTAAGG     480

CGGAAGCTGC CTTAAATCTT GAGGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTTAG     540

CTTCGATTGG AGGAATTCTT CTCTTGGCAG CTTTGGTTTc CTTGGTAACT TCCAGCATGT     600

TTCAGGCTAA AAATTATGCC AATGTAGTCA CGGTTACGGA AAAAGACTTT ACTGAATTTC     660

CTAAGAGTGA CACCAGTAAG GTTCCTATCC TAGATAGAAG TACTGCTGAA AAAATTGGAG     720

ACCGCTACTT GGGTTCCCTA ACCGATAAGG TGTCGCAATA CGTAGCGGCA GATACCTATA     780

CCCAATTGAC AATTGATGGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCCTA     840

TCAAATGGTT TAACAATCAA GCCAAGGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA     900

CTGGAAATGC GGATTTGGTG GACTTGAAGA CACCAATCAA GTATTCAGAC TCGGAGTATT     960

TTAACCGTGA TGTCAAACGT CACCTGCGCT TGAAGTACCC GACCAAAATC TTTAAAACTC    1020

.CATCTTTTGA GGTGGACGAT GAGGGCAATC CTTTCTATGT AGCAACGGTT TACCAAAAGC    1080

AATTTGGACT TGCTGTTCCT CGTCCTGCTT CAGTCATTAT CTTGGATGCT ACAAATGGAG    1140

AAACCAAGGA ATACAGCTTA TCAGATGTTC CAGAATGGGG GGACAGGATC TATCCAGCAG    1200

AGGAAACCAT TGAGCAAATC AACTACAACG GCAAGTACAA GGACGGTTTC TTGAATGCCA    1260

TGATTTCCAA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA    1320

ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATGC GGATGAGAGT AATCTTGGTT    1380

TCATCCTTGA AAATATGCGA ACAGGAGAAA TCACTAAGTA TAGCTTGGCT TCTGCGACAG    1440

AAGAATCAGC CCGTGAATCA GCAGAAGGTG CTGTTCAGGA GAAATCCTAC AAAGCAACCT    1500

TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATG    1560

CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCAGTCGA GTACCAAAAT GTTATCGTTG    1620

CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAACGACCTT GAAATTGACA    1680

ATGCAACGAC AGAAAGCATC AATGGAGTAG TAGCAGACCT CAAATCAGCT GTTATCAACG    1740

GAGACACTGT CTACTTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT    1800

CCGATGACCT TCCTTACCTT GAAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAAAGACA    1860

ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAGAAAG TATATGTTAT    1920

AATAAGGTAA ATTAAGCCG                                                 1939
```

(2) INFORMATION FOR SEQ ID NO: 311:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 907 base pairs
            (B) TYPE: nucleic acid

1339

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          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear


      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGAGTAG AAGTAAGCCA ATTAAATAAT GAGAAAGTTT          60

CATACCCCGT CCTTTCATGT AGATTTGGTA TCGAAAGATA TCTGCGGATA TAAATGTAAC         120

ATTATTTTTC TAATCTGTCA ATAAAATTTC TGACAATTTA ATAAATACAA CAAGGAGAGA        180

GCAACAAGAC TTTCTCCTTT GTTATCCTAT TCTAAAATGT TTTTACCTTA ATCTGATAAA        240

ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTTAGC TTTTGAAGCA        300

TCTGCTAGGA CACTGGCTGG GTCACTAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTTT        360

TAATTTAGTA ATTCTTCAGC AGTTTTAAAG ATTTCTTTGA TAGTATAGCC TTTTTTAGTT       420

CCTAAGTTAA AGATTTGAGA AGAACTGTCT TCTTGAAATA GGTAGTTCAT TCCTTTAACA        480

TGAGCCTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTCACGTGTA        540

TCGTAGTCAT CTCCAAATAT TTTTAAGCTA TCATTTTGTC CCAATGCGGT CTTGTTGATA        600

TTTGGAATGA TGTGAGTTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTTCAGCC        660

CCAGCAACAT TAAAGTAACG GAAAATAACA TATTTCCAGT CGTAGCGATT GGCCATCCAG        720

TAAATCATTC GTTCGCCCAT CAGTTTTGTC TCTGCATAAG GGTTGACAGG GTCGAGCAGG        780

GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAAGAG        840

AACATGATTT TTTGAATGCC AACTTCAGAT AAGACTTTGA GAACTTGGTT CATACCAGCA        900

ACGTTGG                                                                  907
```

(2) INFORMATION FOR SEQ ID NO: 312:

```
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2170 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear


      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAAATATCT TTTGTACTAT CTTGGGCATC CAAGAAAAGC AATTGGGCAA          60

TAACAGAGTT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA         120

GAAGACGTGA GTAAATATCG TAAGAACGTT CTCCACGGCT TGTTTGTTCA ATAACTACAG        180

GAATCATTCA TTTCTCCTTT TGAGTTTTAA TTTTGTTGGT CAAATGACTG AAGATAAGAC        240
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                                1340
TATTATAATA TCTTGGTCAA AAAAGGTCAA ATTTTTGCTC TGCTTTCATT AGACAGAAAC     300

AAAAACCCAA CCTCCTTTCG TGACTGGAAA TACTTTTCCA AGTCATTCTT CTTTTCGATC     360

TTATTTTGTA CCGAACAAGC GGTCTCCAGC ATCTCCAAGA CCTGGAACGA TATAACCGTG     420

TTCGTTCAAA CGTTCATCCA AGGCTGCTGT AAAGATTTCT ACATCTGGAT GAGCTTCTTG     480

AAGGGCTTTT ACACCCTCTG GAGCAGATAC AAGGCAGACA AATTTGATAT TTGATGCGCC     540

ACGTTTTTTA AGAGAATCAA CAGCCAAGAT TGCTGAGCCA CCTGTTGCCA ACATTGGGTC     600

TACTACAAAA ATTTGACGTT GGTCAATGTC CTCAGGCAAT TTCACCAAGT ATTCAACTGG     660

TTGAAGTGTT TCTTCATCAC GGTACATACC GATGTGGCCA ACTTTAGCAG CTGGAACCAA     720

GTTCAAGAGA CCATCAACCA TCCCGATACC TGCACGCAAG ATTGGGACGA TGGCCAATTT     780

CTTACCTGCC AATTGTTTTT GAACTGTTTT TGTAATTGGT GTTTCGATTT CCACATCTTC     840

TAGTGGAAGA TCACGAAGTA CTTCATACCC CATCAACATT GCAATCTCAT CTACTAGCTC     900

ACGAAAAGCT TTTGTAGAAG TATCTGTACG ACGCAAGATT GACAATTTGT GTTGAATCAG     960

TGGGTGATTA ATAACTTCAA TTTTTCCCAT TTTTGGAATT CCTTCTTTCA ATTTATTCTT    1020

CTTATTATAC CAAAAAACGG TTTAAAAATC TTTCTAAACC ATTTATTTTT GATAATTTTT    1080

ACATTAGATC AGCCTCTTTA AGAGCTGTCT GTACTGTCTC AAGTGGTAAA TGGGTCAATT    1140

CTGTCCCTTT TTCTTGATAA AGGTATTGGG CGTAGTCGTC CATTCGGTAC TGGTTGATAT    1200

AAACCACGCG CTTGCAGCCG ACCTGAAGCA ATTGTTTTGT ACAGTTGAGA CAAGGAAAAT    1260

GGGTTACATA GGCTGTAAAG CCTTTGGGAA CACCACGCTC AGCACCTTGA AGGATAGCAT    1320

TGACCTCAGC GTGAAGGGTG CGAACGCAGT GGCCTTCAAT GACCAAACAT TCGTGATCAA    1380

TACAATGCTC AGTCCCTGAC ACCGAACCAT TGTAACCAGT GGAAATAACC TTATTATCTT    1440

TTACCAGAAT CGCGCCCACT TTAGCACGTT TACAAGTGGA ACGATTCGCA ATTAGTAGAG    1500

CTTGGGCTGC AAAATACTCA TCCCAGGCCA GTCTTTTTTC AGTCATCTCT TTTCTCCTTT    1560

TTCTCTATTT TTTAAAAAAT GGTAAACCTA AATCTGCAAT CTTTTCAGCT GGTACCTTCA    1620

TGCCATCCTT GATCCATTTT AGAAGGACAG AGACGATGGC TGAGCTCCAG AAGGAATGAA    1680

GATAAGAGCT GACACCTTTT GATTTCCCAT GGTATTTTTC TAGAAATTCC TGCATGGCTT    1740

GGACAAAGAT TTTTTCCAGA TGGTAATCCA AGGCCAATTG AATTACTCTA GCTTCCTTTC    1800

TGGCCTCCCG GAAAAGGTGA ACCCAAACCA AATAAAGGTC TGTCTTTAAA TCGTAATGAT    1860

GCAGCTGTTC CATAATATTG TGGACAGTTC GTTTAAAGAC GCTCTCTAAA ATTTCCTCTT    1920

TGGAGTCATA ATTGCGATAA AAGGCCGCAC GCGAAACACC TGCACGTTTG ACCAATTCAG    1980

AAATACTAAT CTTGGTCAGT TCCTTTTTTT CCAAGAGTTG CAAGAGGGCT GTTTCAATGG    2040
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1341

CTTCTCTGGT TAATAAATTG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT   2100

CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTCACAACAG ACGGATGATG   2160

CTTTTGTTTC   2170

(2) INFORMATION FOR SEQ ID NO: 313:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 539 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG   60

AGGACATTCA TATGTCACGT TATACAGGAC CATCTTGGAA ACAAGCTCGT CGTCTTGGCC   120

TTTCACTTAC AGGTACAGGT AAAGAATTGG CACGTCGTAA CTACGTACCA GGACAACACG   180

GACCAAACAA CCGTTCTAAA TTGTCAGAAT ACGGTTTGCA ATTGGCTGAA AAACAAAAAC   240

TTCGTTTCAC TTACGGTGTA GGTGAAAAAC AATTCCGTAA CTTGTTCGTA CAAGCTACAA   300

AAATCAAAGG CGGAATCCTA GGTTTCAACT TTATGCTTCT TTTGGAACGT CGTTTGGATA   360

ACGTTGTTTA CCGTCTTGGT CTCGCGACTA CTCGTCGTCA AGCTCGTCAA TTCGTAAACC   420

ACGGTCACAT CCTTGTTGAC GGGAAACGCG TTGATATCCC ATCATrCCGC GTAACTCCAG   480

GTCAAGTGAT CTCAGTTCGT GAAArATCAT TGAAAGTTCC AGCAATCCTT GAAGCAGTA   539

(2) INFORMATION FOR SEQ ID NO: 314:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 667 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTTGC TCCTTCTCTA CGGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT   60

CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTTTCTCT GCCGTCGTAT   120

AGGAAACAGC TACCCTTGTT GGGGTTTCAT TGTATTCTCT TTCAAGTTTC TTAGGTCTAA   180

CAGGACCTGG ACCTGGTCTT GATCCACTTT CTTCCGCTGG AGAAGAAGGT ACATCTTGAC   240

TTGGATGACT TGGAACACCA GGAGTTTCTC TTTGAATCTC ATCTGCTGGA GAAGCTGGTA   300

1342

```
CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTTCT CATAATCTCC TCTACCGTTG        360

ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTCATT TGCAGGAGTG CGAACTACTG        420

CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTTACTTT TTCTAAATCT CTCAGAATCT        480

GCTCTTTAAA GCGTAATTTC TCTTCTGCTC TTGACTTTTC ACTCAAAAGT TTTTCCTCCT        540

TGTTGAGAAT CCATAATATT AGAGCTGAGA AGTCCAAAAA AAGCAATCTA TGATACTTTT        600

CCTAACGGAT TTTGTCATTT CCCAGACCAT ATCATACCAT GTTTCCCCTG CAAAGGTTGA        660

CTGGGAA                                                                 667
```

(2) INFORMATION FOR SEQ ID NO: 315:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1483 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```
GGGAAGCCAA GGTATTTTAT CGGATGAAGT TGTTACTAGT TCTTCACCGA TGGCTACAAA         60

AGAGTCTTCT AATGCAATTA CTAATGATTT AGATAATTCA CCAACTGTTA ATCAGAATCG        120

TTCTGCTGAA ATGATTGCCT CTAATTCAAC CACTAATGGT TTAGATAATT CGTTAAGTGT        180

TAATAGTATC AGCTCTAATG GTACTATTCG TTCCAATTCA CAATTAGACA ACAGAACAGT        240

TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA        300

CAGAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCGGT        360

AGGTGATGGG ATTCATGATG ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA        420

AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAACT TATTTAGTAA AAGAAATTGT        480

TTTTTTAAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAATTC TAAATGGTAT        540

AAATATTAAG AATCACCCTT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTGC        600

GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA        660

CGGTGCTTTG AATGAAGAAG GAACTAAAGC AAAAAATCTA CCACTTATAA ATTCTTCAGG        720

TGCATTTGCT ATTGGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG        780

TTATCAAGGG CATGCTATTC AAATTGCAGG TTCGAAAAAT GTATTAGTTG ATAATTCTCG        840

TTTTCTTGGG CAAGCCTTAC CCAAAACGAT GAAGGATGGG CAAATCATAA GTAAGGAGAG        900

CATTCAGATT GAACCATTAA CTAGAAAAGG TTTTCCTTAT GCCTTGAATG ATGATGGGAA        960

AAAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA       1020
```

1343

```
ATTAGTAACA GCAATTGGCA CACACTATCA AACATTGTCG ACACAGAACC CCTCTAATAT      1080

TAAAATTCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT      1140

CACTGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGTACA      1200

TTATCGAGAA AGCGGAGCAG CTTTAGTAAA TGCTTATAGC TATAAAAACA CTAAAGACCT      1260

ATTAGATTTA AATAAACAGG TGGTTATCGC CGAAAATATA TTTAATATTG CCGATCCTAA      1320

AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAaTwT TTAGGAAAAG TATCAGATAT      1380

TACTGTAACA AAAAATGTAA TTAATAATAA TTCTAAGGAA ACAGAACAAC CAAATATTGA      1440

ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT                       1483
```

(2) INFORMATION FOR SEQ ID NO: 316:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2453 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

```
CCTGAACGCT TTTTTATAAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAAGCG       60

ACGCGAATTA AAATTCATTG CATACTCCAT CGCTTCTAAA AAACTCATTT TTGAAAAGAC      120

GTTAAAATCA TCTAAATTCT GACTCCAATA TAATAACAAA ACCAATCCCA TAATATCCTC      180

TGGTTGATTA TTCAATAAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG      240

CAACTTTTTT TCTTCAATTT GAGTTTCTTT CCTTAGGGCA TGCTCAAAGT CTATAATATA      300

AATATTATTT CTATTATCAA TAAGTATATT ATTAAATGAT AAATCTCTAT AGGAAAGATT      360

ATATTTGGAG TTTATTATCT CCATATAATC AATTAATGTT AAAAACCAAT CATACGAGCC      420

ACTAACCATA TTATACTCGC TTAATTTATC TGCAATAATA AACTCAAATT CCACAAAATA      480

CGAATTCTTT ATGTAAAAAT CGTTAAAAAC TTTTGGAGTA AATTCCTCCT TTTCCAATTC      540

TACTAATATT TCTCTTTCAT TTATTAAACG ATTCACAGAA TCTCTATTTG TAAAATCAAC      600

CAACGATAAA TCACTAGCTT CTTTTAATAA AGAATAAACT CGCTTTTGAG TATTAAATAC      660

TTTATAAACT CCACCTTTGG CATTTTTAGA AATCACTTCC AAAATAATAT ATTGATCAGG      720

AATAGTGTTA TATCTTGGAA TATAGTAATC CCTTATTGGA ACATTCACAT TTGAAGGGAT      780

TTTCTTATCT CTTTTATCCT TGAAAGTGCT ATCTTTTACG AACTCCCCAT ATCTGTAATA      840

TACAACCTCG CTAAGTTGAA ATCTGAAATC TGATGGTATG TTTACACCCT TTACACCTTT      900
```

1344

```
ATACAATATT TCTAATTTGT GTAACAAACG TTGAAACTCT TTATTATCTT TTGGATAAAT        960

TGTAATGAAT TTCCCGACTT GTGAATAACC ATTAAGCCCT GTATTTTGCA AAGAAAGTTC       1020

TTTAATGCTA ACCAAAATTT TGAAATTTAT CTTCTTCTCT CTAGAAAATA TAAAATCAAA       1080

GAATTTTTTA GCAACCAAAT TAGCATTTAA TATTGAAGCG CTCAGGTGTA TTTTAAATCC       1140

CTTAGATTGG GTGATATTAG ACGGCAAATT ATATAACCAA TGTTCATCAC TAAAATTATC       1200

ACTAATTTTA TATTCTAATA ATAAATTATG GTATGCGTCT TCTATTTCAG TTTCATAGTC       1260

CAAATAGTTT AAATACTTTT CGTAATTCAT ATTAAGAAAT CTTCTCCATA AATTTTTAGA       1320

CCATCATTTA AAGCCAAACA ATTTAAAGCG TGATAATAAA TGTTGATAAT CAATGTAACT       1380

TTCAGTCCTC TATTTTGTAA TTCCTTCACC AATAATTTTA TGCTATATCT ATTTTCTCGA       1440

GGCAATTTAT AGGACTTCAA GATAAAACCA TAAAAGAGAT AAGTATTATA ATCTGACAAT       1500

CCAGTTTCAG AATAATTTTT TAGAAAAATA TCTAGTGATT CTGATAATTC ATCCGGAATA       1560

ATTCTTTTAA CATCGTATTT ATTTTTCATA TCGGCCACTC TTCCTTAAAA AGCTCACAAT       1620

AAAATTTTAA ATTTCTATAC AACAATCCGA GAGTAGTCTC ACAATTTGAA CATTTCACAT       1680

CACTCTTAAT ATATAAAAAA TGAATTAATC AGAAACCTCT GACTAAGATT TCCTAATTAA       1740

TTCACTTTCT ATATCATAGT AAGGAATTCT ATTATCCCTA ATTGAAAATT GAAATTTTAT       1800

GTTTTATATA TTAACAATTA TGCGGATTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA       1860

CTATGTGCCC CAGAAGGCGA TGCAACGCTA TTTTGAATTG AAAGAGCATA ATCATCCATA       1920

TCATTTAAGT CACGGATTAG CAATGCTTCC TTCTCTCTTC CGACAATTCC AAATTTTCTA       1980

ATTACCTTTT CAGGATTATC AAAAAATTCT CCAACAACTT CCATATTTCC TTGAAGTTCA       2040

TTCAAGAAAG CTTTCATTTG ACTACTCATT ATATAGCTCC TTTTCTATTA CTTTATTTGG       2100

AATCAAAACT TACTTGTACA TTGGAAACAC CTCTATTCTA CGCTTTCATA TTGCTGCATG       2160

ACACTTTCAA AATCAAATTG CTAAAAATAA TTTTTTAAAG CTTAATTTAG ATTTAATTAC       2220

ATATATCTCA AAAAATTGTT TTGAAATTAG TAAATTAAAA TAGGTTTCTG TACTTATAGG       2280

AACTAGTTAT AAAAACTTCG CCCATCATAA AATATCTATT TAAGTAAAAC AAAAATTTTA       2340

TAATTTTTTG ATTTTTAAGT GACTATAATC TCCTATCTAT AAATACCATT CGCAGGACCT       2400

GGATCAATCC CTCTAGCCAT CTTATGAACT TGAGTTCCTC CAGACAGTCC CGG             2453
```

(2) INFORMATION FOR SEQ ID NO: 317:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1049 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

```
CCAATTTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTTGCCAT        60

TCCAGCAgTA CTCAAAAACT TTACTTATCA CCAGTTTTAG ATGGCTTTAA CAGCGAAATT       120

ATTGCTTTTA ATCTTTCTTG TTCGCCTAAT TTAGAATAAG TACAAACAAT GTTGGAACAG       180

GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC       240

CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACGC       300

AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTTCT TTGGCATTTT GAAATCGGAG       360

ATGTTTTATG GTTATGAGAA GAACTTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG       420

GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT       480

GTGCAATACA GAACTAAATC CTTCGGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC       540

ATTTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT       600

GGATGTAACT TACTATATTC ACAATGTTAT CCAGTGTTTT TTCTCTAATA TTTAAGGAGT       660

GTTCTGTTTC TCGAATAAAT TCTTCAAAGT TTAACCCGTC AACTTGTTCC TGAACAAGAA       720

AATAATCATC CACGATATAA AATTCATCAG TTAAATTAGT AGTATAACTT TTATCGGCTA       780

ATTTTTTTAG CATGTGAGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTTCAG       840

CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTTGCCCG TCCGATTTTC       900

TAATTGCCCG ATAAACATTT CCTTTATTTG ATCTCTTAAT AATTTTTTCC ATTTTGTATT       960

TATTTATTGC AGAGTCCTTA CTTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT      1020

CTTCTTCTGA AAATAAATCC ATTTTCCGG                                       1049
```

(2) INFORMATION FOR SEQ ID NO: 318:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 776 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```
TTAGTTGGTT AGAATCAGAA AATCGCCGAA GTGGTTATTT ATTTTTGAAT AAATTTAACG        60

AACCAATTAC AGCAAGAGGA GTTGCTCAAC AGTTAAAAAA TTATGCTGAT AAATACAAAA       120

TGAATCCTAA AGTAATTTAC CCTCATTCTT TTAGGCATTT ATTTGCTAAG AATTTTTTAG       180
```

1346

```
CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAACT ATAGAAACTA    240

CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACAACAAAA TATTGTAGAT AAAATTGTTA    300

ATTGGTAAAA AATAACAGGT GGTCAAACTG ACTACCTGCT ATTTTTGTGA TTATGGCTCT    360

TATTATGGGA ATATACCTAT GAATTGGGTT GTTATAAAAA TAAAAGATAT TTTTTCAATA    420

AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATTA ATAATAAAGG TGTTAGAATT    480

ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTACTACATT    540

GATACACAAT TCATCTCCTC TGAGCAAGTT TATTTAAAAC ATAATCAGCT AATAACACCT    600

GTATCAACCT CTTTAGAACA TATTGGAAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT    660

GTTGTGGCTG GTGGATGTAT TTTCCAATTA ACACCATTCG AAAGTGCAGA GATGATGTCA    720

AAATGTCTAT TATGTAACTT GTCCTCTCCG TTATTTTATA AACAATTGAA AGCAAT        776
```

(2) INFORMATION FOR SEQ ID NO: 319:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 658 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```
TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA    60

ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTCGATC AGGATGATCT    120

GGACGAAGAG CATCAGGGGC TCGCGCCACC GAACTGTTCG CCAGGCTCAA GGCGCGCATG    180

CCCGACGGCG AGGATCTCGT CGTGACCCAT GGCGATGCCT GCTTGCCGAA TATCATGGTG    240

GAAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGGC TGGGTGTGGC GGACCGCTAT    300

CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC    360

CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTCGC AGCGCATCGC CTTCTATCGC    420

CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGGTTCGA TGTCGACAGC CCGCCTAATG    480

AGCGGGCTTT TTTTTCCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGGC AGTGCAAATC    540

CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCCCG AACTGCAGGA    600

GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTC GCGCGACCGG ATCGATCC     658
```

(2) INFORMATION FOR SEQ ID NO: 320:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1475 base pairs
        (B) TYPE: nucleic acid

1347
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```
CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA        60

AAAGAAAATT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG       120

CTCATTCTAC AATTGACTCG AGGATTATTC ACTTCAAATT AGAATTTGCA AATGAATTTT       180

TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA       240

TTATTGACGG TAAACCTTAT GTTCTGGAAC AAACTTATAT GAGTACCGAT GTTATTCCAG       300

GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTGAAGGA AAGTTAGGAT       360

TGCATATTGC CAGTGCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC       420

ATTACTTGCA GCTCCTTCCA ACGGAACCGG TATTTGAAGT AGAACAAGTG GCTTATTTGG       480

ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA       540

ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAATGTG AAAATGAAGC CAATCTTTTA       600

CAGACTCTAG TTTAAGAAAA ATTTAAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG       660

GTTTCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGATC GTTGTATCCA TCATGTTGAA       720

AAAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATTG TTCACCTGAT CTACTTCTTA       780

TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTCTTACA CTGACGAGAA GTTTTTGAGT       840

CTTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCTAACAA       900

ATTGCTAGAA ATGAATTTCA ATCTCCCAAT TTATTTGTTC ATATCTTCTT TTAATATATT       960

AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTTATT TTTTATTTTT CATTACGAAT      1020

AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA      1080

AGGAGAAAAA ATGAAAGTAG AAAATATTTC GTATAGGGTG GATCATCGTA AATTGTTTGA      1140

TAATATTTCT TTTGATACTT CGAGTTCAGA CGTGACATTA ATTACTGGTA AAAATGGTAC      1200

AGGAAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCTAAAA      1260

TATTGTTAGA AATCGATTTG ACTATCCTGA TCTATTTGTC CTGTTCTTAT TTCATTTCAC      1320

TATATCTCAA ATTGAGTATG ACGAAGTGCG CTCCCATGTC CTGGGAACGC ACTTTCTTCA      1380

TATTTTTCAT ATTCTTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA      1440

CTAATCATTT TTACAGGATG AGATTTACAG CAGAG                                 1475
```

(2) INFORMATION FOR SEQ ID NO: 321:

1348
```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 560 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTC ATGCCCTCAT        60

ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA       120

TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATACA CCACTATGAA CTCGTTGGTC       180

TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTTGTTTTT GGTGCGGGTT       240

TGAATTTAAA AAATTTGTTA TGTAGTACCT AATCTAAGGA ATTAGAACAA TGCCTCTAAT       300

TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTTGAAAC AGCTCTTCTT       360

TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTTT       420

TTTCTAAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG       480

CTGTTACACA AATTAGCTAA AAAArACTCT GGGGTTGGGA AAGGAAGATA AGAAaCGTAT       540

TTAGCCCATA ATCTATAAAG                                                  560

(2) INFORMATION FOR SEQ ID NO: 322:
                         \
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 643 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCGGCC ACCGCTGCCT ATCCTCGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT        60

AGACACGGTG CGGTACGACC TCGTACTACT TTCGCCGACG GCCTCGTCCG TTGTCATCCA       120

CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TGCGTGTCGG       180

GCCTGAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCCGGGTTTG ATGACGAGGG       240

TACACCCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA       300

TCGGGCGACT GGAGGAATGG CGCCTTTTTC CGGTTTGACC AAAGTGGCAT CACATGGTGT       360

CAAACCTGGC TCAAGATGTA CGCATCTCAA GGCGGAAGGG GAATCGTCAC AGGAAGGAGT       420

TACCGGAGTA CCCGCCGAAC GCACCGTTTG GATAGAGCAT TTTTCTGCAG CGAACTACCA       480

TTCAGGTCGA GCCTTTTTCA GGTCTGGCCT TGCCTGGGTA GGCAGCCGAG AAGAACTCTT       540
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1349

ATATCCCTTA ATGCCTTTCA CCATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTGTG   600

GCATTTAGAC GGTCAAACGG AACGAGCACG TAGGGTACTG TGC   643

(2) INFORMATION FOR SEQ ID NO: 323:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 780 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TGCGAGTTGA   60

AGTCAAGAAG AGGAAAAAAA CAAAAAGGAG AAATACTCAT GGCAGTAATT TCAATGAAAC   120

AACTTCTTGA GGCTGGTGTA CACTTTGGTC ACCAAACTCG TCGCTGGAAT CCTAAGATGG   180

CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAAACTGTAA   240

AATACGCTGA CCAAGCATAC GACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT   300

TGTTCGTTGG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTCAG   360

GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAACTCT TACAAACTGG GGAACAATCC   420

AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTCGAAG   480

TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAAACAACG TGCGCGTCTT GAAAAATTCT   540

TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTAtTG ACCCACATAA   600

AGAGCAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA   660

CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG   720

TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT   780

(2) INFORMATION FOR SEQ ID NO: 324:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 624 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAACT   60

AGGTGTCGAA TTGGAACTAT CTCCCATGAG TTTTGATAAT GTACTGGCTA GTGTTCAATC   120

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                                  1350
AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT        180

TGACTTTTCC ATTCCCTACT ATACTGCAAA AAATAAACTC ATTGTCAAAA AATCTGACTT        240

GACTACTTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTTC        300

GATTCAAGAG ACGATGGCGA AAGATTTGCT ACAAAATTCT TCCCTCGTAT CTCTGCCTAA        360

AAATGGGAAT TTAATCACAG ATTTAAAATC AGGACAAGTG GATGCCGTTA TCTTTGAAGA        420

ACCTGTTTCC AAGGGATTTG TGGAAAATAA TCCTGATTTA GCAATCGCAG ACCTCAATTT        480

TGAAAAGAG CAAGATGATT CCTACGCGGT AGCCATgAAA AAAGATAGCA AGAAATTGAA         540

AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGGAATTA GACAAACTCA        600

TTGAGGAAGC CTTATAAGCA TCCA                                              624
```

(2) INFORMATION FOR SEQ ID NO: 325:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1237 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

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TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT         60

CTAGTGCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAAC AGTCCCGGGG TGAACTGACT        120

TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG        180

GAGGCAGACT TGGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAGCTTC        240

AGTCCTGCGA TCTTACTTGC TATTCATAAG GAGTTGTTTC AAGATATATT TGAACCCTCG        300

ATTCCGGTAG GTCAATTTCG TCAGACTAAT ATCACAAAGA ATGAACCTGT TTTGAATGGT        360

GAAAGTGTTG TGTACTCTGA TTACTCCATG ATTCAAATGA CCTTGGATTA TGATTTTAAT        420

CAGGAAAAAC AAGTTGCATA TGCGACACTA ACCCAGGCGG ATATGGTTAA AAAAATCCAG        480

CATTTTATTT CAGGAATCTG GCAGATTCAT CCATTTCGCG AAGGAAACAC TCGGACGGTA        540

ACGGTATTTT TGATTCAGTA TCTTCGTGAG TTTGGTTTTG ATATTGATAA TACACCATTT        600

CAGCAACATT CCAAGTATTT TCGTGATGCC TTAGTGTTAG ATAATGCAAA GATTTTACAG        660

CGACGTCCTG AGTTTTTAAC AGCTTTTTTT GAAAATCTCT TGCTCGGTGG TCAAAATGAT        720

TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTCATAATC CTAATACTGA        780

GTAAACATTG AATTTTAGGA AAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT        840

CAAAGTTTGG CTCTTTGTCA ATTGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC        900
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1351

AAAATTTCGGC CTTTCCTTTT TGATGTTCAG AGCGATAAAA ATCCGGTTTT TTGAAGTTTT   960

CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT   1020

CCAGTTTGGC ATTAGAATAG TGTAGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA   1080

GGAAGGGTTT AAAGACAGTC TGAAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA   1140

GTTCGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC   1200

GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAG   1237

(2) INFORMATION FOR SEQ ID NO: 326:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 461 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATTGGAACA   60

AGTGCATTTT CTTTTAGTCA AAAATTGAAA AAGCTAACCT TTTCCTCAAG TTCAAAATTA   120

GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAAACT AACATTACCA   180

AAATCGGTTA AAACATTAGG AAGTAATCTA TTTAGACTCA CTACTAGCTT AAAACATGTT   240

GATGTTGAAG AAGGAAATGA ATCGTTTGCC TCAGTTGATG GTGTTTTGTT TTCAAAAGAT   300

AAAACCCAAT TAATTTATTA TCCAAGTCAA AAAAATGACG AAAGTTATAA AACGCCTAAG   360

GAGACAAAAG AACTTGCATC ATATTCGTTT AATAAAAATT CTTACTTGAA AAAACTCGAA   420

TTGAATGAAG GTTTAGAAAA AATCGGTACT TTTGCATTTG C   461

(2) INFORMATION FOR SEQ ID NO: 327:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1436 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTTAAACAAT   60

ATATCAAACA TCAATGACTA GAATACTTGC ATCATCCTTC TTTCCATAGA TTGGATCAAT   120

AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTTCAAAA GTTTTATTTT GATTATTTTG   180

1352

ATAGAATTCA TAAAAGCCAT CGCTCATTAA AACAATTTGT TCACTAGTAA CATCTATTTG   240

ATTAATAATA GCATGGTCTA AAAATCTCTC ATCCAACGAA CCTATCCAGT ACCCACTCGG   300

TTGATTAGAT AATTTTCTGA TTTTTTGTAA AATAATTTTT TTATTTAAAA CACTATTTGT   360

ACCAATTGAA TCTTTTATCT CATTTTTCCC TTTTTCAAAT AAGTTATCTA CTCTATGATC   420

AGTTATTTCC ATTTCGTTTA CTAACATGAC GCAGTCACCT AGCATCATAT ACTCCAACTT   480

TTTTTCTGAA AGTTTAGCAA ATATTGGTAA GCGATAATAT AGTATATTGA AACTAGAATA   540

GTACACCTCT ACTTCTAAAA CATTGTTAGA AATCGATTTG ACTGTCCTGA TTGATTTGTC   600

CTATTATTAT TTCATTTTAC TATACTCTGT TAATTTATAT GAGTTTAAAC CGATTTCATC   660

TTTAACCTCG AGTAAAGCAG TTTCAAATAT TTGTTTAAGA GTTTTTGATT CTTTACAATT   720

AACCGACAAA CTTTCTGATA AAATATGTAC AACTTCTGAG ACTGAATAAC CTATCTCCTC   780

TTTAGAATTA TATAAATCTG TAGCTCCACC AATAATCCAA AAATACTGAT TTTGTGAACC   840

TACAATATCC TCATTTTCTA CGGAACTTCC TTGTATCGAA CAAATTTTAT TTATCTTTAC   900

CATAATACTT CAACCCTTTT AGTGTCAAAA GTAAACCAAT TCCTGTCACT GTTAAGAATA   960

GTTCCATAAT CTTATTCGAA CCAGTCTTTG GTAATTTTTG TTTkACATCT ACTATyTCTT   1020

TAGATTTATT AATATGATTT TCAGTTTCTC TGCCATCTCC AACTATTTTA TAGTTTACTT   1080

CTTCTGTCTT ATTATCTTGT TTATTGTCGA TCTTGTCATT CATTTGTCTA TTATCTTTAC   1140

TTGAGTTAAA CTCTCCGTTC TTCTGGTTAC TATCAATTAC ATTATTTGAA TTAGATTGTT   1200

TTTCCTCTTT GTTTTTTTCT TTTTCGTTTT TATCACTTAA ATTATTTGTT ACAATTTTGT   1260

AAAGCCCATT CTCCGTTACA ATATTGAAAT TACCATCGCT ATCACGTATA ACAGGTTCTT   1320

TCCCATTTGC ATTAGATTTG ATGAATGATA TATACTTACC GGATAAATTA TAAAATTGGT   1380

TATTTAAAAC GGTTATTTTA CCCTTTGAAT CCTCAATAAC AATTCCTTCT TTACCC   1436

(2) INFORMATION FOR SEQ ID NO: 328:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 646 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA ATCTCAAATG GTTCGTCAAT GGTTTCTGAT   60

ACGTATTTTC CGTCTTTCTT CCGTTGCTTG ACACACTCTG TGAGGAGATA TTCGATTTGC   120

CCATTGACTG AACGAAAGTC GTCTTCTGCC CATGATGCGA GTGCAGCGTA TAACTTTGTT   180

1353

GAGAGTCGAA GGGGGATCTG CTTTTTTTTA GCTTCAGCCA TCTTTAGTAA AGGCTTCCTG   240

TGTTGACAAT TGGTTGTGCA TCATGATTGC CACAAAGAAC GACAAGGAGA TTTGAAACCA   300

TGGCAGCTTT TCGTTCTTCG TCAAGTTCTA CCAATTCCCC TTCATTGAGC CGTTCTAGTG   360

CCATTTCAAC CATTCCTACA GCACCATCTA CAATCATCTT CCGTGCATCA ATAATGGCAG   420

ATGCTTGTTG GCGTTGAAGC ATAACGGCAG CAATTTCTGG AGCATAAGCT AGGTAAGTGA   480

TACGTGCTTC AAGGATTTCC AAGCCAGCAT CCTCAACACG ACTTTGGATT TCTTCACGAA   540

TACGGGTAGC AACAATTTCG CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC   600

CCGGAGTATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC   646

(2) INFORMATION FOR SEQ ID NO: 329:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1653 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTGCAGGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAGGC TCTTTTTGAG   60

GCAGGAGCGG ATGCGATTGT TATTGATACT GCACATGGTC ATTCTGCAGG TGTCTTGCGT   120

AAAATTGCCG AGATTCGTGC TCATTTCCCA GATCGGACTT TGATTGCTGG AAATATTGCT   180

ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGTGTAG ACGTTGTTAA GGTTGGTATT   240

GGACCAGGTT CTATCTGTAC TACTCGTGTG ATTGCTGGTG TTGGTGTTCC GCAAGTAACA   300

GCTATCTACG ATGCTGCAGC TGTTGCGCGC GAATATGGTA AAACGATTAT TGCTGACGGT   360

GGGATCAAGT ATTCTGGAGA TATTGTAAAA GCACTTGCTG CAGGTGGAAA TGCTGTTATG   420

CTTGGATCTA TGTTTGCTGG AACTGATGAA GCTCCAGGCG AAACTGAAAT CTTCCAAGGA   ·480

CGTAAATTCA AGACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAAGC   540

GACCGTTATT TCCAAGGTTC TGTCAATGAA GCAAACAAGC TTGTTCCAGA AGGAATTGAA   600

GGTCGTGTTG CTTATAAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT   660

CGCTCTGGTA TGGGTTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA   720

TTTATTGAAA TGTCTGGTGC TGGTTTGAAA GAAAGCCATC CTCATGATGT GCAAATTACT   780

AATGAGGCAC CAAATTATTC TATGTAAAAA ACAATGAAAA GAACTCCAGT GAAAACAGGA   840

GTTCTTTTAC AATGTTGTCA ATTTCCATTT ACAGCAGCTT TACCATCCTG AATAGTGAAG   900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TTGTTGTTGT GATAAAGGTT   960

TGGATTGATT GAGAAATCGT TTCTAATAAT TTTAACTGTC TAGTGTTGTC AAGTTCACTC   1020

ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT   1080

TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTTGGCTTCC GAAACTAGCA   1140

TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT   1200

TTAAATAAAT CTCTGGATCT ACTTTTTTCT AAAGCAATTT TGAAAGATTC GGATAAGTTT   1260

TGTTTGTCAG TTATATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA   1320

GAGAGTTCAA AATGTTTCTT ACGCCCAAAT GATTCTAGTT TTTTTATGAA ATCTAAGCGG   1380

TGATTCATTA CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT   1440

TCATCTATTT TTTGAGCTGA TTTTAGGTAA GTGTTTCTTT GCTTTAGGAT GTGGTTATAA   1500

TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT   1560

CGTCGAATCG AAGGTGCTCC TTTAATTAGT TGTAAATCTT CAGGAGCAAA TAAGACAACA   1620

TTCATGTGTC CTACATAATC TGAAAGGCGT GCC   1653

(2) INFORMATION FOR SEQ ID NO: 330:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1340 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTTTGTT AGTTTAAAAT TACTCCCATT CTTCTTTTCC   60

AAACGTACAA TATATCCAAA ACCATTCAAA ATACTAGATT CTATTTTTTA TAATATCACT   120

AAATCCACCT AATTATAGGA CGTTTTCAGA TTTTTAGTCC CAGTCCCAGT ACCGGAGAAA   180

TATTGTTTTA ATATAATATC TCTTTTTGTC TTCTAAGCTC TTAAAAGCAA AAGAACAAGT   240

AAAGAGTCAA GACAAGGATA AAAAGTCCAT ATTAGGGCAA ATAAAAAGCT TTAAGACAGA   300

TGACAAATCT AAGTCAAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC   360

GGTCTTCGGA CTGCCTTTAT TTTTTTATCC ATTTTTCAAA TCAAATTTAT TCAGACTATA   420

TATGCACATA TACACTTAAA TTCATATAAA AACATGGCTT GTAAAAAATT ACTTTAATCA   480

CAATAATCGC ATTTAAAATT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGGAAGT   540

TTTCCCTTGT ATCTTTTATA ATAGATAGAA AATTTGCTGG CAGATGAATA TCCAACAGAT   600

TCTGCTATCT CTTTTATAGG TAGTTCAGTG TTTAAAAGAA GAGTTTCAGC TACATTCATT   660

1355

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CTTTTTCTTT GAGTGTACTC TGTAATGCTT TGACAATATT TTTCCTTAAA TAAATTTTTT       720

AATTTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTTAC ATTCGTTGCA       780

AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTCAATT       840

TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCCTTT       900

GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC       960

ACTCTTTCTA AGGCCTTTGT AAGTATTATT TGATTCGGTT GAAGCAAGGT TGAATAAAAA      1020

GATTCTGGAT TAATGTTAAT AGATGCTAAA TGTTTTTCTA TTAGCTCTTT TTTAAAACCm      1080

ATGGAAACAG CAAGATAACA ACAATTCTCG TGTAATAAAA AAACAAAATT ATCTTTTATA      1140

TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATTAAACTTT      1200

TCTCCGTTTG CACTGACAAT GTAACTTGAA TAAATTGAAA CATAGTCTGA CATACTATAA      1260

GTGCTATTTT GAACTACTTC CTCTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG      1320

CCTCCTTCAT AAAACCGGTA                                                  1340
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(2) INFORMATION FOR SEQ ID NO: 331:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 607 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

```
TATGTTCGTG ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAACTT        60

GTAAAAGAAA CTCTTTTTTC ACCCGTAGTA GTTGATAATG GGTTTGATCC GGCCTTATTT       120

GAAATTGAGA AAAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTTAT       180

TTTGCACATA AAGAATTGGA TAAATTGTTT TTTCATGATG AACGTCTTCA ATTGGAATAT       240

AGTGATTTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA       300

GAATTTTTAG CCAATGATCG AATAGATTTC TTTTTCCTAG GTGATTTTAA TGAGGTTGAA       360

ATTCAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTCAG       420

TATTGTCAAC CTTATTCTAA TATCCTTCAG GAAGGTATGG TTCGGAAAAA TGTGGGACAA       480

TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC       540

ATGGATTGAA TGAATGGTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC       600

CGGGAAA                                                                607
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1356
(2) INFORMATION FOR SEQ ID NO: 332:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 900 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAAATACC GAATTTTGTT TTGTCCTCTA TTTCAACATT GTGAATCGCC TCAGGCAGAG   60

AACCGATACT AAAGATATAA CCAAAATAGT TGTCATTTGC TTTACCGATA TCAATCTTAT   120

TGGTTAAATC AAAATCCAGT TCGTCAATTG CGCCATCGAT GTCTTGATTG ATTTCCAAAA   180

GTTTTGTAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACTTAGGA ATGTAGTCTC   240

TCTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCCATC TCCACCAAAC ACAACCACTG   300

CATCATACTG CTCACGAGAA GCTTCTTCAG CAAAATGTGT TGCATCCAGC GCTTTTTCGG   360

TAATTTTGGT TTCAACATAT TCAAAGTATT CTTTTGCTTT ATTCTCCAGC TTTTCTTTGT   420

AATCCAAAGC CTTCTCGCCA CCAGAAGTAG GGTTGATAAT TACCATTGCT TTTTTCATTG   480

ATTTTATCCT TAATTTTAAA CAGAAATGTT TACATTTCGT CGTATGCAAG TAAATGTAAT   540

CCTATTATAC AATGAAAATA CAGAAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT   600

TTATTCTATT TTCCCATCGC CTAACTACAT CCTTTAAGGG TTCATCCAAG TAAGAATAGG   660

CCTTATCCTT GATCCAATCA GGAATACCGT AAGCTGCCTC TGCTAwGCTA CAAGTGATTG   720

CTGCGAGAGT ATCACTGTCG CCACCAAGTG AGATGGCATT TCTTATCGCA TCTTCGAAGT   780

CTCTACTTTC AAGAAAGGCG ATAATGGCTT GAGGGACAGT TTCCTGACAT GTTTCGTTAA   840

AACGATAGTT AGGACGGATT TCATCTAAAG TTTGAGATAG ATTGTAATCG TATTCTTTTT   900

(2) INFORMATION FOR SEQ ID NO: 333:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 533 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTTCTGGC ACACTGGTCT TGGAATACGG CAAAACCTCT GAAAATATCT ATGCTGGAAT   60

GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAAA CAGCCAAACA   120

TGCTTTTGAT CGCGGACAGA TTGGCAAAAT ATGGGTGGAA TCGAAAACGA CCTCAAGGGC   180

1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATTG AGGAATTCGC TGGTGAGTTC   240

AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA   300

CTGCGCAGaA GcATTAACAG AAAGGAAGCC TATGACCTTT AAACTTCTCA GCCAAGAAGA   360

ATTCATCCAG CATACCTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC   420

AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGG   480

GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC   533

(2) INFORMATION FOR SEQ ID NO: 334:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 544 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAACT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAGATAAG   60

ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC   120

TCAAAACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG   180

AGGTTGCAGA TAGAACTGAC GAAGTCAnnA ACCACACCTA CGGCAAAGTG AATCTGAAGT   240

GGTTTGAAGA GAGTACAACT TGTCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC   300

ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTTA TCTTGATGGA ATCTTAGCAG   360

TCAAGGATTC TCAAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG   420

AGCAGATTAT AGACTATCAG GGAGCTTGGA TTATGCCTGG TTTGGTCAAT TGTCACACCC   480

ATTCTGCAAT GACAGGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA   540

ATGA   544

(2) INFORMATION FOR SEQ ID NO: 335:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 349 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAGT AGGGGTTCCT TTTTTGTATA TTTTTCAAAT AACGCCTCTA   60

1358

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CACTATTTGT AGCAAATTCA CCAACTACAG TTGTATCTTA GTTAAAATAA GTTAGAATAT        120

GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCATCT AAGGTATATT CAAAATACAA        180

AAGTTGACCA ACTAGATTTC TGAATATCCT TATATATCCA TTCTTAAAAT TGGTTTAAAT        240

AGCGTAGTCT TTTAAACTAG TTTTGAGAAT CCAAAAAATC TTCCTACATA TGTAAGAAGA ·      300

TTTTTTAGTT CAGAATGATT AGaTTTAGCT AATGGATACC TATCCTACC                    349
```

(2) INFORMATION FOR SEQ ID NO: 336:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1206 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```
CTCCGATAAC CACACCAGCA ATGGAAATAA TTCCATCGTT AGCATCAAGA ACACCCGCAC         60

GCAGGATATT TAAACGACCT GCAAAATTTG AATCAATTTC GTGATTTGTT TCTGACGCTA        120

AATTTCAAGT TCAAGTTAGC CATCAAGAAG TCTTCTCTGG GTGACTTGTA GTCCAAGCAT        180

TTTTTAGGAT AGTTGTTAAT CCACTTTTCG ATGAATGCGA CTTCTTTGGG AGTCATTTTC        240

TTGGTTCCCT TAGGTAACCA TCTACGAATG AGCCTGTTGT GATTCTCATT AGTTCCCGGG        300

ATCCTCTAGA GTCGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC  .     360

GATGACTGGG GAAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT        420

CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG        480

CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTTC        540

ACACCGCATA TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC        600

CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC        660

TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAGTTTT CACCGTCATC        720

ACCGAAACGC GCGAAACGAA AGGGCCTCGT GATACGCCTA TTTTTATAGG TTAATGTCAT        780

GATAAGGATG GTTTCTTAGA CGTCAAGTGG CACTTATCGG GGAAATGTGC GCCGAGACCC        840

TATTTGTTTA TTTGTCTAAA TACATTCAAA TATGTATCCG CTCGTGAGAA AATAAACCTG        900

ATAAATGCGT CAATAATATT GAAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTCGC        960

CCTTATACCC TTTTTTGCGG CATGTTGCCT TCCTGTTTTT GCTCACCCAG AAAACGCTGG       1020

TGAAAGTTTA AGATGCTGAA AAATCATTTG GGTGCACAAC TGGGGTTACA TCCAACTGGA       1080

ATCTCCAnCA GCAGTTAAGA TCCTCTGACA GTTGTACACG CCGCAAGAAC TATTCCCGAT       1140
```

1359

GAATGAGCAA CTTTTAAAAG TCCTGCGAAT GTTGGGGCGG TAATAATCCC CGTGTTGTAG   1200

GCCCGG   1206

(2) INFORMATION FOR SEQ ID NO: 337:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 813 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT   60

GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTCGCCCTT ACCGTATGTC AAAAGATTTT   120

TACCGTGAAC TGGGCTTAGA CACTCCTATG ATTAACTTCA ACGGATCCCT TACTCATTTA   180

CCAGACCAAG TTTGGGATTT TGAAAAGTGT TTGACTGTAG ACAAAAAATA TCTGCTAGAT   240

ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA   300

TTCTACATTA CAAATCCCAA TGAAGAAATT GCCAATCCCA AACTATTTGG TGTAGAAGCT   360

TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCTAA CTGTATCCTC   420

TTGCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAG AAATGAACGC CTTCTACCAG   480

CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCCAAAA   540

GGTGTCAACA AGGCCTTTGC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA   600

GATTTGATTG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG   660

GGTTATGCCA TGAAAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTTCC   720

CTTACCAACG ACCAAGATGG GGTTGCCAAA ACCCTACAAG ACTTATTCTT ATAACCTATA   780

CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA   813

(2) INFORMATION FOR SEQ ID NO: 338:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 683 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAAGGAGA TTGATGATGG   60

```
                                 1360
ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTCG TACAGAGGTT CTCGCTGGTT        120

TAACAACTTT CTTTGCAATG AGCTATATTC TCTTTGTAAA CCCACAAATA CTTTCACAAA        180

CAGGAATGCC TGCTCAGGGC GTCTTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT        240

TGATGATGGC TTTTTATGCT AACTTACCTT ATGCCCAAGC GCCAGGTATG GGACTCAATG        300

CCTTCTTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA        360

TGGTCTTCAT CTGTGGGATT ATTTCATTGA TTATTACCTT GACAAATGTT CGTAAAATGA        420

TCATTGAATC GATTCCCAAT GCTCTTCGCT CAGCTATTTC AGCTGGTATC GGTGTCTTCC        480

TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTTGAAATT CACGATTGAT CCAGGCAACT        540

ATACTGTTGT AGGAGAAGGG GCTGACAAAG CTCAAGCAAC GATTGCAGCA AACTCTTCAG        600

CAGTTCCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG        660

CCATTACTAT CTTCTTTGTC ATC                                               683
```

(2) INFORMATION FOR SEQ ID NO: 339:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 852 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```
CTACTTTACA TGGAAGTAGT CACTGAATTC CAGTTAGAAA TTACTTTGTA ACTACGTTTT         60

GAGGAGGAGT AAAATGCTTT CCTACGTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT        120

GTGTCTGTGC TCTCCTAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT        180

ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTC CACCAGTATC GATTATTTAA        240

TTATTTTAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAAATGG CATATTTATG        300

CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGGCGAG TTTAGTTGCT GCTTATGTCG        360

TTAATTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG        420

GGATTCGCTT TGCAATTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA        480

GATTAGAACA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT        540

CTGGCGGAGA TAATTTAGGT ATCTATATAC CTTATTTTGC TTCGTTAGAT TGGTCACAGA        600

CCCTCGTGGC CTTGCTTGTG TTTGTAATCG GCATAATTAT CTTTTGCGAG ATTAGTCGGG        660

TGTTATCCTC TATTCCGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCATTGTGC        720

CCTTAGTATT CATTCTACTT GGACTATACA TCATGTATGA AAATGGCACG ATAGAGACTT        780
```

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTTAG CCCGAGCTCA AATCAGCTCT   840

CTGATTTTCA GA   852

(2) INFORMATION FOR SEQ ID NO: 340:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 754 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATG   60

GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT   120

CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACATCA TAACAACAAG   180

AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT   240

AGAGAACAGA GTTAGTAAAC CTAAAATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT   300

ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC   360

AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCCTTGT AAAGCCTGAT AGATAATGCC   420

ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAAATCATC TGACCAAATA AGATCAAAAA   480

CAAGGCAAAC GCAAAGAGGA GCTGCAACCA AAACTGACTA GGAGACTTAG CATCTGATGG   540

GAAATAAGTC CACGACTCTT TTCGACGCCA TAAGCCTTGT TAAAAGCTTT TTGCAAGAAA   600

TTCATAGATT TTGAAAAACT CCATAACGCC GATAAAACAG AAAAACTCAA TAAACCTGTT   660

GAAGGTTGCG TCAAGACTTC TCTGGCTATT TTTTCCACAC CTTCATAGAG GCTTGGGGGG   720

CAGACGTCTT TCATAAAGCC CAAAAATTCT CCCA   754

(2) INFORMATION FOR SEQ ID NO: 341:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 707 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGCACAAG AAGTCAGGAT   60

TTTTATGCAG GTTGGGCGCT TCATCAGACA GGGAAGATTT ACAGCGACTA TTATGGAAGT   120

1362

```
CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC      180

TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG      240

ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT      300

CTTGCTTTTG GTGGAGGCTA TGCCGACTCTT TTAGCGCTTC CTTTCTTATT CGCAGCCTTT     360

AGTTTAGTTG CGGCTTACCT AAGCAATCCA AGCCATGATA AGGGATTTGT ACGGATTGGG      420

CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGCTCCTGTT TATTGCTGTA      480

GTGAGTTTAG GCTTGTTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTTAT      540

CAGTTTCTTG CAGTGGCTTT AGGTTTTTCA CTTGTCTTTT ATCCAACTGC CTACTATAGT     600

GCTGCAACAG GAAGTTTTGG GGATGCGwTT AGTGGTATTC GTTATCCTAT TGACAGTATT     660

CGCTTTGATT TTACTTCTAA AATTTTAGAG AATATGTTTT TTTAAGG                    707
```

(2) INFORMATION FOR SEQ ID NO: 342:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 762 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```
GGATTTTGAA AAACCATACC GATTTGACGA CGTATATTCC AAACATTTTC CTCAGTCAAA      60

CGTTGGCCAT CAATTACAAT CTCTCCGGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA      120

ACCGTCGTTG ATTTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC      180

ACGTGAAAgT AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA     240

GATTTTTTAC ATCAATTATT GATTTCATTT CGAACCAAAT GTCCCTTTAA ATACATAGGC     300

ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAAGTAG     360

AACTTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA     420

AGTTTTAATT TTTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACCAGTTT CAACCAATAA     480

AAGCCTTAAA CCTGTCACAG CTAACTCACG ACAGATAATC ACTGCAACAA TCCAAGCCGG     540

AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAACT TATCCGCCAT     600

AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC     660

TAAATAGTCG GTAATACTGG CAACAGCAAA GATAATAGCT GCAACTATAT GACTCTCTAT     720

CGAATTTCCT ATCGTTAAAA TAAAGATAAA AATAGGTATA AA                        762
```

(2) INFORMATION FOR SEQ ID NO: 343:

1363

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 482 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CTTTTGATAC ACTTAAACTA TGAATACAAA TCTCAAGCCC AAACTTCAGC GTTTTGCTTC          60

TGCGACTGCC TTTGCCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT         120

CAAGTGCTGC AACCGTCATT CTTTTGACTT GGCGAAATTT GGCTATGTCA ATCTAGTCCC         180

TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT         240

AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA         300

AACTACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTCTC GCAAACTACA         360

AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT         420

CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCACGACT         480

TC                                                                       482
```

(2) INFORMATION FOR SEQ ID NO: 344:

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 520 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TTTATTTTTA TAAAGTCAAT ACCTGTCTTT ACTTTTTCTT AAAAAAAGTT TATTATGTTC          60

TTTAAGGAGG TGTAAAACAT GAAAATAAAT AATAAACTCG TTGGAGAACG TATTCAAAAT         120

ATCCGTTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAAA         180

GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTTACCAA ATAAAGAAAA CCTACTAAAA         240

ATTGCATCTA TTGGAAAAAT GAGTGTTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT         300

CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC         360

TCTTTACACG ATGATATAAC AAATAAAGCG TTACAGATCG CTCAAAATAC CATTTCTAAG         420

ATTGATTATC AAATTTCAGA CGAAACGATC AAAAAATTTA TTGATTTAGC TATCGAACAA         480

TCGAGAGATT TGCAAGGAAA TTTGTTGAAA AATAACGGGT                               520
```

1364
(2) INFORMATION FOR SEQ ID NO: 345:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1003 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```
GCATCAAATC CGCCATCAAA GAAGTTCTCT GGATTTACCA AGACCAGTCA AATAGCTTAG      60

AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG     120

GAACCATTGG TGAGCGCTAT GGTGCCGTTG TTAAGAAACA CGACATTATC AATAAGCTTC     180

TCAAACAGTT GGAAACCAAT CCTTGGAACC GCCGCAATAT TATTTCGCTC TGGGATTACC     240

AAGCTTTCGA AGAAACAGAT GGGCTGCTCC CGTGCGCCTT TCAGACCATG TTTGATGTTC     300

GGCGTGTTGA TGGGGAAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC     360

TGGTGGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC     420

ATTTTGGCTG GAAGGTTGGG AAGTTCTTCT ACTTCATCAA CAACCTCCAT ATCTATGATA     480

ATCAATTTGA ACAAGCTCAG GAATTGCTCC GTCGGGAgCC GTCAAACTGC CAACCACGCT     540

TGGTTTTAAA TGTTCCTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT     600

TGGTGGATTA TGACCCTGTT AAGCCACAGT TGAAGTTTGA CCTAGCTATT TAAAAGAATA     660

GAAAAAAGAA GTTGAGAATA ATCCCAACTT CTTTTGTTTC TTAACGTGAT ACGCGGCGAC     720

GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTTT TTGCTCTTCT GGTTCGATTA     780

CTTTCTTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTTCCT GCGACACCTG     840

TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG  .   900

CCAGCCTCCT CAAGAGGTCA CATTTTTCTG ACTGACCTTT TTGTGTTATA ATAATAGTAA     960

CGAAAAAATG GGAATTTTTC AAGGAAAAAA GATGAGAACA AAA                      1003
```

(2) INFORMATION FOR SEQ ID NO: 346:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 750 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```
CCGCACGTAC TATTCCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGGC GCAACTGGTC      60
```

1365

```
TCAACGCCTT TGAACGCCTC TTGGTCGGCT CTTCATCTGA ATACATACTC CGCCATGCTA        120

AGGTCGATTT GCTGGTTGTG AGAGAACAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG        180

CCCCTAGCTC CTTTTTGTTT ACGATTTATT TCTCTCTTTA TGGCGTTCGT AAGCCTTGAG        240

CTGGCGCTGC AGTTCCTTTT TAATAGCAGG TTCTGGAGCA TATTTTTCTT CCCAATTATC        300

TGGTTTTAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTGCCATCTG GAAAAATTTT        360

CCCCATATTG GCCTGATGGA CAATATCAAA AATACGTTCT GGGTCCACCC CCATCAAGAC        420

AAAACTGCCG TAGGTGAAGT AAAGCGTGTC AATCAAGGCA TCCACTTGCC CTATCAAATC        480

TTGCTGAGCA GGTGTCTTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAAG        540

TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAAACTCCAC        600

CAATTCTTCT ATTTTAAAAC CAGCCCTATG GGTTGCACCC TCTAAATCCC AAGCTCGAGG        660

TTCTTCTTGG GTTCGTTCAT CCATCATGTG GTGGAAAGTC TTGACCTTAT TGAAATGATA        720

GTCACGGCTG ACAAAGACTT TTTCTGAAGA                                        750
```

(2) INFORMATION FOR SEQ ID NO: 347:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　(A) LENGTH: 596 base pairs
　　　　　(B) TYPE: nucleic acid
　　　　　(C) STRANDEDNESS: double
　　　　　(D) TOPOLOGY: linear

　　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```
CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA         60

TGTTAGAGTC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT        120

GTTGATCTTG AGGATAAGTG TACTTACCGC CAACTTCCCA GATAAATGGA TGGAAATCGT        180

ATTGCAAGCG ATCTTTTCGC ATTTTCCAAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA        240

AGTTAGACCA GATATCATAG TGAACTGGGA TAATGACTTT GGTACGCAGA TTTTCTGCCA        300

TACGAAGAAG GTCGATAGAT GTCAkTTTGT CTTGGATACC TACCGGATTT TCACCATAGT        360

TATTCAAAGC AACATCAATT TTAAAGTCTT TACCATGTTT TGCAAAATAG TTTGAGAAGT        420

GAGAATCTGC ACCATGATAG ATGGTTCCAC CTGGTGTTTC AAAGATATAG TTAACAGCCT        480

TTTGAGCCAT TTCTTCATCT GTAACAGCCA AGCCAGCAgT TCACCGCCTG TCTCATCAGC        540

ACCGTTCACT GGGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCTACTG CATGAA           596
```

(2) INFORMATION FOR SEQ ID NO: 348:

1366

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 673 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```
CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA        60

GCTCCTCCAT CAGTTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA       120

ATCACAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAGTT TGTCATTGTT GATATCGACT       180

GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA       240

CCAGCACCGT AAAGAACAAC CCATTGGCCT GGTTCAACTT TTGCTTCTTT GATAGCTTTA       300

TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA       360

ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTCAG CCATACCACC GTCTACTGAG       420

TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTCGCAA       480

GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC       540

ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCCTGGG       600

ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTCGGTGT GGCAAACGCC CACAGTATTC       660

ACTTCTACAA GTG                                                         673
```

(2) INFORMATION FOR SEQ ID NO: 349:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

```
GTACCCTACA AATGCTTTAC AGTATGGGTT GAGGGTGGTC AATGGAACTA TGGAGTAGGT        60

TGGACAGGAA CTTTTGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT       120

GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAAC CTGAGGCATG GGCTAGAGCT       180

TCCCTCACCA AGATTCCG                                                    198
```

(2) INFORMATION FOR SEQ ID NO: 350:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 891 base pairs
        (B) TYPE: nucleic acid

1367

```
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG        60

GACCAATCCA CTACTAATCC TAAGAACAAA ACACTCAAGA GAGCAGAAGA GAGAGGTTCA       120

CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG       180

AAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA       240

TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA       300

ATCATCCCCC ACCCAACCGT AGGAACAAAA CCATAACGCT TAGCAAAAGG TTGGGGCAAG       360

ATAACATTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGCGGCGTC       420

ATGGATAACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC       480

AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTTGAT AAACCAAGCG ATTGTAAAAG       540

AGGATAAAGA CAGGGCTAAT AAACTGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATTCT       600

ACACAGAGAT AGAAAAAATA CTGAACTGAA AAAATCCCCA AAATAGCATA GGCTAAAAAG       660

GGCAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA       720

GACCAAATGA GTACAAGACT CCCTGCCAGT GTCAAACGCA TAGAGGTAAT CCAGCCCGAA       780

GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAAATTC CACAGATTCC CCATATTAAG       840

CCGGATAGGA GCGAATAAAT TTTTCCGTTA ACAATCTTTT TCTGATACTG A               891
```

(2) INFORMATION FOR SEQ ID NO: 351:

```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 325 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GAAAGCGTTC AATAGAACAT TGCTTTTTTA TTTTTAGAGT AAGCTAAGCG CTTCAGCATC        60

TGCGATGATG GTTACATCAG GGTGATTTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC       120

TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTCGAC TCACCGTAAG CAAAAAGAAT       180

AATAGACTTG GCATCCAAAA TGTTTTTAAT CCCCATTGAA ATAGCTTGGG TTGGGACGTC       240

TTCAATCTTG GCAAAGAAGC GTGCATTGGC TTCGATAGTA GACTGGTCAA GTTCTACTAG       300
```

1368
ATGCGTTTGA CTGTCAAATG GAGTG   325

(2) INFORMATION FOR SEQ ID NO: 352:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 344 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCAGT TTGATGATTT TTGATAAGCA TGCGAATTTA AAATACAAAT ATGGCAATCG   60

CAAGTTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC   120

TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCG   180

AGTCAGTAGA TCCGTTTACT GGCGAAATAA ATAAGAGGAA GTAACGTnAA GTGCTTTAGC   240

ACCTGCTCGG GAAAGTGGTG CGCGAGGAAG CTATTTCAGG ATGCTTTGGC CCTGGCCGGT   300

AGAAGCGTTA TAGCCGCAGA CTACGACACT TCACACTGGT GGTT   344

(2) INFORMATION FOR SEQ ID NO: 353:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 692 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT   60

TGGACCTGTT CCCTTCACTC TGCAAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA   120

CCGAGAGAGG CTGTACTTTC TGCTGGACTC TATCTTCTTC TAGGTGCTAT CGGTCTTCCT   180

GTCTTTGCAG GAGGTGGAGC TGGTTTTCAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT   240

TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGTT   300

GTTAAGATTT TTCTTGCAAA CCTCTTGGGT GATGCCCTTG TCTTTGTCGG CGGGATTCTC   360

AGCTTGCATT TCCTAGCTGG AATGGCATTT GAAAAAGCTC TTGCTGTGGG GGTTCTTCCC   420

TTTATCATTC CAGACCTTGG CAAACTTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT   480

CAACGCCTTA AAAATCAGGC TTACTTTACT AACTAAAAAA GGATATCGAG TTATCATGAC   540

TCAATATCCT TTTCTTTTAT TTTGAAAACT TATACTCAAT GAAAATCAAA GAGCAAACTA   600

GGAAGCTAGC CGCAGGCTnG CAAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA   660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC   692

(2) INFORMATION FOR SEQ ID NO: 354:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1005 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA AACGCATCCA GAAGATTTTT TCGATAATGT CGGACCTCTT   60

GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTTCC ACTTGATGAA GGAAATTGGA   120

GTTAATTCTT TCCGCACTTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT   180

GAGCCTGATC CAAAAGGTAT TGCTTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC   240

CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTTAC CAGTGGAACT TCTTCAAAAA   300

TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTCG TGAAGTTTGC CAAGACTGCT   360

TTCACATGCT TTGGAGATAA GGTTCATTAC TGGACAACTT TCAATGAGCC AATGGTCATT   420

CCAGAAGCAG GGTACTTATA TGCTTTCCAT TATCCAAATC TAAAAGGAAA GGGAAAAGAG   480

GCCGTACAAG TCATCTATAA TCTAAACCTT GCTAGTGCAA AAGTGATTCA ACTATATCGC   540

TCATTAGAAC TTGATGGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA   600

AGTAATTCTC CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAAGTC   660

TTCTTGAATC CAGCTGTTAA AGGAACTTTC CCAGAAAGAT TGGTAAAACA GCTAGAGAGA   720

GATGGCGTGT TATGGAGTCA TACCGAAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT   780

GATTTTCTTG GAGTAAACTA CTACCATCCA AAACGTGTTC AAGCACAAGC AAATCCTGAG   840

GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT   900

CGCATGAATC CATATCGTGG TTGGGAAATT TTTCCGAAAG CCATTTATGA TATTGCTATG   960

ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA   1005

(2) INFORMATION FOR SEQ ID NO: 355:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 973 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

1370
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```
CCGACAAGCA ATATTAAAAA GAGTAAACTA TTAACTAGTT AATTAACCGG TTTATTACTT        60

TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAGAATG AAAATTAATA AAAAATATCT       120

AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTTGTTCC TATGAGCTTG GACGTTACCA       180

AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG       240

TCAAAAGGCA GAAAACTTGA CACCAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA       300

ACAAATTGTT ATCAAGATTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA       360

TTACTATAAT GGCAAGGTTC CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA       420

TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCAATGAA ATCAAGGGTG GTTATGTCAT       480

TAAGGTAAAC GGTAAATACT ATGTTTACCT TAAGGATGCA GCTCATGCGG ATAATATTCG       540

GACAAAAGAA GAGATTAAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC       600

AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT       660

CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA       720

CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC       780

CTATTGGAAT GGGAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAATCC       840

AGCTCAACCA AGATTGTCAG AGAACCACAA TCTGACTGTC ACTCCAACTT ATCATCAAAA       900

TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCTT ATCAGAACGC       960

CATGTGGGAT CTG                                                          973
```

(2) INFORMATION FOR SEQ ID NO: 356:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 843 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```
GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCG        60

TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG       120

CACCAATTCG TCAAACTCAT TGCCACGGTC CAAACCACCT GCAATCAAGA CGACCTTGCT       180

GTTGTCAAAT CCTGACAAGC TTTTTGAGTA GCCAAGATAT TAGTTGATTT ACTGTCGTTA       240

TAGAATTTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG       300

GCTGAAAGAG TTTCCTTGAT GGTTTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA       360
```

1371

```
GTCGCAAGGG CATTTTCCAC ATTGTGGCTA CCTGGAACAC CGATTTCATT CGCTGCCATG        420

ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA        480

AGTGTTGAAA ATGGTACAAC AGTGGCTTCT GTCTTGGAAG TCAAGTCTTT TGCCAAGTCT        540

TGATTAAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCTGGAT ATTCCACTTG        600

GCTGCTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA        660

ATAACCGCAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGGAAAGA AGAAAGTTCC        720

ATAACAAGCG TGTCCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA        780

TTCCCTGATA AAAGACCATG TTGGCCAGCA GCAGTCAAAA CTTCCCGGGn TCCTCTAGAG        840

TCG                                                                     843
```

(2) INFORMATION FOR SEQ ID NO: 357:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 807 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

```
TTTTTTTTAT ATTTTTTTTA TTTATTATTT TTTGGCAAAA AAGACCAATT TGCTTTGGAG         60

CATTGCTTCT GCATTAAATT GTCTATTTTT GCTCGTGCTG TTACGCTCTT TGTATCATGT        120

ATTAACTAGC AAGTGCAACT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGGTTATG        180

ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCGTAATG CTAACCAAGC TAAACACGAA        240

GTACTTGAAG TACCTGCATC AAACATCAAA AAAGGGATTC CTGAAATCCT TAAACGCGAA        300

GGTTTTGTAA AAAACGTTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT        360

CTTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA        420

GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGGAATT        480

GCCATCCTTT CAACTTCTGA AGGTTTGCTT ACTGATAAAG AAGCACGCCA AAAGAATGTT        540

GGTGGTGAGG TTATCGCTTA CGTTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA        600

GCAAAATTAG GAAGTTGGAG AAGTTTGTTT ACAAACAGGC CAACTTATCT ATTTTGCACA        660

GTTCTTAGAG CGTGTTCAGT TCAGCTCTTG AGCTAAGTAA GTATCTGAAC CCCGTGAAAA       ·720

CTGGCCGTGC TGGCATGTTC GGGTAACAGG AGAnAATAAA CATGTCACGT ATTGGTAATA        780

AGTTCAGCTA AGGCCTTCGT AAAAGTT                                           807
```

1372
(2) INFORMATION FOR SEQ ID NO: 358:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 653 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATTT TTGTCCAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATTGGCTCTC   60

TTAACCATCT tTGAACAAAA TCCTCAGGCT CAGGTCACTA TTTTCGGTGC CTTGGGTGGC   120

CGTATTGACC ATATGTTGGC CAATGTCTTT CTGCCTAGCA ATCCTAAGTT GGCACCCTAT   180

ATGCATCAAA TAGAAATTGA GGATGGGCAA AACTTGATTA CTTATTGTCC AGAAGGAATC   240

AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC   300

CAAGTATGAG TTGACAGAGG AAAATTTTTT CTTTAAAAAA GTGTACGCTT CTAACGAATA   360

TATAGATAGG GAAGTGTCGG TAACTTGCCC AGATGGTTAT GTGGTCGTAC TGCATAGCAA   420

GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTATTATT AATTGCCAAT CTAGCTGGTC   480

TCTTTCTGAT TTGGCAAAGG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGGAGG   540

ATCAGGCAGA TCATTTGTCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAAGCCA   600

GCCAGTTAGA CCAAAAAGAT TTGGAAGTGG TTGTCAGCGA CCGTTTGCAA GAA   653

(2) INFORMATION FOR SEQ ID NO: 359:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 641 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCGAGCCAT CGTGTGCAAT   60

GACTCTTCCC GATGTAATCT TGTTCATAGT CCTTTGATGA ATATGTTCAA GCTGTAGAAG   120

GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGGCGAGTT GACCAGTCAG GAAACAGATG   180

GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCCGCATTTA CCTAAAACAA GCCTTCCAAG   240

AAAATAGCAA CCTCCTAGAG CAAGTGGTAG AACCCTTGAC TATTATCACT GGTGGACACA   300

ACCACAAGGA CCAGTTGACC TATGCTTGGA AAACACTTTT GCAGAATGCG CCACATGATA   360

GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCGCGAGAT GGAAACGCGT TTTGCCAAGG   420

1373

```
TCAACCAAGT AGGAAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAG GGTAAAATTG        480

CTACGGATAA GGCTCAAAGT GACTATCTCT TTACTGTCAT TAACACAGGC TTGCATGATA        540

AGGTCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTCAAG GAATTGCACC        600

CAACAGAAGG CTACAAAAAG ATGGCTGCTC TTATCTTGCC G                           641
```

(2) INFORMATION FOR SEQ ID NO: 360:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1958 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

```
CCTCAAGGCC AATTTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA         60

TTTGCCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTTTAGA TGGCTTTAAT        120

AGCGAAATTA TTGCTTTTAA TCTTTCGACT TCACCCAACT TAGAACAAGT ACAAACAATG        180

TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TGACCAAGGC        240

TGGCAATATC AACACGATTC TTATCATCGG TTCCTAGAGA GTAAGGGAAT TCAAGCATCT        300

ATGTCACGCA AGGGCAACAG CCAAGACAAC GGTATGATGG AATCTTTCTT TGGCATTTTA        360

AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA        420

GCCATTATAG ACTATATTGA TTACTACAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA        480

CTTAGTCCTG TGCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTTGG        540

GGTCAGTACA AAACTCTTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTTCT        600

CTCAAATCGA GTTTTTACTC AATTTTCTTA CTTGATTGGG ATTGAAATTC CAATTAATTT        660

CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT        720

CAAGAAAAAT TCTTGAATGG TTTCGATTTC AGGCTCACGA ATAGCACGGT GTTTGTTTGA        780

GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAAATA ACATCTGTAT TCCCTGCAGA        840

ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCGAGTG        900

TGAGTTTGTC GTATTGATAA GCTTCATAAT ATTTCCTCCG ATTTTCTAAT TCTATTATAG        960

CACTTTTTGA ATAAAGTCGC TTGATTTATA CTCAATGAAA ATCAAAGAGC AAACTAGGAA       1020

GCTAGCCGCA GGCTATACTT GAGTACGGTA AGGCGACGCT GACGTGGTTT GAATTTTATT       1080

TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTTCCAAG ATTCAATGGC CCATTTATGG       1140
```

1374

```
CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG      1200

TTTTCTAGTG GCTTTTGTAC TTCTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG      1260

TAGTAGTAGG TATCACGATG ACGAGAATAG AAATATTCGT CAGCTTGTCC GTAATAGGTA      1320

CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA      1380

TTTTCACCTG CTTCAATTTC TCCACATGGT AGGAACCAAG CACCATTTGG TTCTTGAACA      1440

AGAACAATTT GTTTTTGTTC AGGATTAGGG ATAACTGCAT ATACGCCATA GCGAGCAATA      1500

TAGTCTGTAT TCACTTTTTT TCTCCGAAAG TTGGGTTTGC CATTGCATTT TCCTCATTAT      1560

CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAAATAG TACACAATGT GGTATAATCT      1620

TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAACAGG      1680

TAGTATAACA GAAGCATCAC ACGTTTTCCA AATCTCACGT AATACCATTT ATGGCTGGTT      1740

AAAGCTAAAA GAGAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA       1800

GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA      1860

AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG      1920

tACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC                                1958
```

(2) INFORMATION FOR SEQ ID NO: 361:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 851 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

```
TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG      60

CTTAGAGAAG CTTTCAAATA AATTTGGGAT AmACAATTCT AATCTTAGGT ATATGATTAA      120

ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAAGGA AAAAATCGTT ACTATTCTCC      180

TGATTTAAAA CAAGAAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT      240

TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG      300

GAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG      360

CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC      420

AGAAATTGTT TAAGAATTAA TGACTGAGTT TTCGTTAGAT CTTCTTTTAA AAGTCATTAA      480

ACTAGCTCGT TCGACCTACT ACTATCACTT GAAACAGCTA GATAAACCAG ATAAGGACCA      540

AGAGCTTAAA GCTGAAATTC AATCCATTTT TATCGAACAC AAAGGAAATT ATGCTTATCG      600
```

1375

```
TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG        660

CTTGATGAAA GTACTCAATt TACAAGCTAA AACGCGACAG AAACGAAAAT ATTCTTCTCA        720

TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCAA GGCCAATTTG AAGGCTCTAA        780

AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCCAGTAA GTACTTAAAA        840

GCTTTACTTA T                                                            851
```

(2) INFORMATION FOR SEQ ID NO: 362:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1168 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

```
GGGTAGAATC GATATCTCCA ATGAGTTGGT tTAGCTGGTG AAACTGTAAA AAGATTTCGw         60

CCAATTCAAG GTTGAGGCAT CGCAAACTAT GGACTGTTTC CTCGTCAGTT CTGGAAAGAA        120

AACGGGATAA GGTTGGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTTT GGAAAGTAGG        180

CATCAGCTGA CAATTCTTTA CAAGCATAGT CCGTTCCATA ACCTGTTAAC AGTTGAAAGA        240

GGAACTGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA        300

CTAAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTTCC TGAAAAAAGA        360

TAAGACCACC ATACTGGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT        420

TTTGGAAGTG ATGATTTGGT AAACTGTTCA TGTGAGTTTC CTTTCTTTTT GTGTTTTTTT        480

CTACACTTAT ACCATAAAGG GGAAACTCTT TTTTGTCTAG TAAAAAACAC CCATTGGGTG        540

AAAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTTG        600

GGGTGAATAA TTGGGGTTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAACTTAC        660

TCATCAACCT TTAGTGGAAA TCCAACTACA TTTAACTATC TATTAGACTA TTACGCTGAT        720

AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG        780

GTAATACCTT TTTGAGGTGC TTTTTGATAT GAGCCCATGT TTTCTCAATA GGATTGTACT        840

CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATACCCAAA CTCTTCACAC AAGAGTTCTA        900

ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTTAATG        960

TTGGTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAAGTC GCTCGTCATC GTCTCTTCGT       1020

AAGTTATTGG AGCGATTAAC TCACCATTTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT       1080
```

1376

ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC   1140

GATAAAAATA AGTATCGAAT CCTGTTTC   1168

(2) INFORMATION FOR SEQ ID NO: 363:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4483 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC   60

GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC   120

GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC   180

TTCAGCAAGC ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC   240

GAGTGCGTCT GAGTCAGCAT CAACGAGTAC GTCAGCCTCA GCAAGCACAT CAGCTTCTGA   300

ATCTGCATCA ACCAGTGCGT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC   360

CAGTGCTTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC   420

ATCAACCAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC   480

ATCGGCTTCA GCATCAACCA GTGCCTCGGC TTCAGCGTCA ACCAGTGCGT CAGCTTCAGC   540

AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCTTCA GCCTCAGCAT CGACAAGTGC   600

CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC   660

AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGCGTCA GCCTCAGCAA GTACTAGTGC   720

ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGCGTCA ACCAGTGCAT CAGAGTCAGC   780

AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCCTCG GCTTCAGCAA GCACCAGTGC   840

GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGCGT CAGCCTCAGC   900

AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCC GCTTCAGCAA GTACTAGCGC   960

CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGCGT CTGAATCGGC   1020

ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC   1080

ATCGGCTTCA GCATCAACGA GTGCGTCCGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC   1140

GTCAACAAGT GCATCGGCTT CAGCGTCAAC GAGTGCGTCT GAGTCAGCAT CAACGAGTGC   1200

GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CAgCCTCAGC   1260

ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCGTCA GcTCAGCGTC GACAAGTGCs   1320

1377

```
TCrGCTTCAG CAAGTACCAG TGCGTCAGCC TCAGCAAGTA CCAGTGCkTC AGCCTCAGCG    1380

TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TGCGTCAGCC    1440

TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCCGCTTC AGCAAGTACT    1500

AGTGCATCAG CTTCAGCAAG TACTAGCGCC TCAGCCTCAG CGTCGACAAG CGCCTCAGCT    1560

TCAGCAAGTA CCAGTGCGTC AGCCTCAGCG TCGACAAGTG CGTCGGCTTC AGCAAGTACC    1620

TCAGCGTCTG AATCAGCATC AACAAGTGCG TCGGCTTCAG CATCAACGAG TGCATCAGCT    1680

TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG    1740

AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCCG CATCAACAAG TGCCTCGGCT    1800

TCAGCAAGCA CCAGTGCTTC GGCTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAACG    1860

AGTGCGTCAC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCACTTC    1920

CGCATCAACA AGCGCCTCGG CCTCAGCAAG TACAAGTGCT TCAGCCTCAG CATCAACCAG    1980

TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCT CAACCAGTG CCTCGGCTTC     2040

AGCAAGTACC AGTGCGTCAG cTTCAGCAAG CACAAGTGCG TCAGCTTCAG CATCAACCAG    2100

TGCTTCGGCT TCGGCATCAA CAAGTGCCTC AGCATCAGCA TCAACGAGTG CGTCAsCTCA    2160

GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGCAT CAGCCTCAGC AAGTATCTCA    2220

GCGTCTGAAT CGGCATCAAC GAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA    2280

GCGTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGCGT CGGCTTCAGC ATCAACCAGT    2340

GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT CAACGAGTGC GTCAGcCTCA    2400

GCAAGTACTA GTGCATCAGC ATCAGCATCA ACGAGTGCAT CGGCTTCAGC AAGTACCAGC    2460

GCCTCAGCTT CAGCAAGCAC CAGTGCGTCA GCCTCAGCAA GTACCAGCGC CTCAGCCTCA    2520

GCAAGCACCA GTGCCTCAGC TTCAGCAAGT ACCAGTGCGT CAGCCTCAGC GTCGACAAGT    2580

GCGTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA    2640

GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGCGT CGGCTTCAGC ATCAACGAGT    2700

GCTTCAGTCT CAGCGTCAAC CAGTGCCTCT GAATCAGCAT CAACAAGTGC CTCGGCTTCA    2760

GCAAGCACCA GTGCGTCGGC TTCAGCAAGT ACTAGTGCAT CGGCTTCAGC ATCGACAAGT    2820

GCGTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCAGCCTCA    2880

GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC GTCAACCAGT    2940

GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCCTCA    3000

GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC    3060
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1378

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ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCG        3120

GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAGTGC GTCGGCTTCA        3180

GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT        3240

GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG        3300

GCATCAACCA GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT        3360

GCTTCAGCCT CAGCGTCGAC AAGTGCGTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA        3420

ACCAGTGCGT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG        3480

GCTTCAGCAT CAACCAGTGC CTCGGCTTCA GCGTCAACCA GTGCGTCAGC TTCAGCAAGT        3540

ACCAGTGCTT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCTCG        3600

GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT        3660

ACCAGTGCGT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA        3720

GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT        3780

ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT CAGCAAGCAC CAGTGCGTCG        3840

GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCGTCAGC CTCAGCAAGT        3900

ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA        3960

GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGCGTCTGA ATCGGCATCA        4020

ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG        4080

GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA        4140

ACAAGTGCAT CGGGTTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGCGTCA        4200

CCTCAkCAAG CACATCAGCT TCTGAATCTG CATCAACCAG TGCGTCACTT CCGCATCAAC        4260

AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC        4320

TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCCTCGGCT TCAGCAAGTA        4380

CCAGTGCGTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGGC        4440

TTCGGCATCA ACAAGTGCCT CAGCATCAGC ATCAACGAGT GCG                         4483
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(2) INFORMATION FOR SEQ ID NO: 364:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2550 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

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GTACCTCAGC GTCCTTCCGC CTCAACCAGT GCGTCCGCTT CAGCAAGCAC AAGTGCGTCA        60

CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCGGCC TCAGCAAGCG       120

CAAGTACCTC AGCGTCACTT CCGCCTCAAC CAGTGCGTCG GCTTCAGCAA GCACAAGTGC       180

GTCAsCTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCGTC TGAGTCAGCA       240

TCAACGAGTA CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCGGCATC AACCAGTGCG       300

TCAGCCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG       360

TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TGCGTCAGCC       420

TCAGCAAGTA CTAGTGCATC AGCTTCAGCA TCAACGAGTG CATCGGCTTC AGCATCAACC       480

AGTGCCTCGG CTTCAGCGTC AACCAGTGCG TCAGCTTCAG CAAGTACCAG TGCTTCAGTC       540

TCAGCATCAA CAAGTGCTTC AGCCTCAGCA TCGACAAGTG CCTCGGCTTC AGCAAGCACA       600

TCAGCATCTG AATCAGCGTC GACAAGTGCG TCGGCCTCAA CCAGTGCATC TGAATCGGCA       660

TCAACCAGTG CGTCAGCCTC AGCAAGTACT AGTGCATCAG CTTCAGCATC AACGAGTGCA       720

TCGGCTTCGG CGTCAACCAG TGCATCAGAG TCAGCAAGTA CCAGTGCGTC AGCTTCCGCA       780

TCAACAAGTG CCTCGGCTTC AGCAAGCACA TCAGCATCTG AATCAGCGTC AACCAGTGCT       840

TCGGCTTCAG CAAGTACCAG TGCTTCAGCT TCAGCATCAA CCAGCGCCTC GGCCTCAGCA       900

AGCACCTCAG CTTCTGAATC GGCCTCAACC AGCGCCTCGG CCTCAGCAAG CACCTCAGCT       960

TCTGAATCGG CCTCAACCAG CGCCTCAGCC TCAGCATCAA CGAGTGCTTC GGCTTCAGCA      1020

AGCACAAGCG CCTCGGGTTC AGCATCAACG AGTACGTCAG CTTCAGCGTC AACCAGTGCT      1080

TCAGCCTCAG CATCAACAAG TGCGTCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA      1140

TCAACGAGTG CGTCTGAGTC AGCATCAACG AGTACGTCAG CCTCAGCAAG CACAAGTGCT      1200

TCAGCCTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCGTC CGCTTCAGCA      1260

AGTACTAGCG CCTCAGCATC AGCGTCAACA AGTGCTTCGG CTTCAGCGTC AACGAGTGCG      1320

TCTGAGTCAG CATCAACGAG TACGTCAGCC TCAGCAAGCA CATCAGCTTC TGAATCTGCA      1380

TCAACCAGTG CGTCAGCCTC AGCATCGACA AGCGCCTCAG CTTCAGCAAG TACCAGTGCG      1440

TCAGCCTCAG CAAGTACCAG TGCTTCAGCC TCAGCGTCGA CAAGTGCGTC GGCCTCAACC      1500

AGTGCATCTG AATCGGCATC AACCAGTGCG TCAGCTCAGC AAGTACTAGT GCATCAGCTT      1560

CAGCATCAAC GAGTGCATCG GCTTCGGCGT CAACCAGTGC ATCAGAGTCA GCAAGTACCA      1620

GTGCGTCACt TCCGCATCAA CAAGTGCCTC GGCTTCAGCA AGCACATCAG CATCTGAATC      1680

AGCGTCAACC AGTGCTTCGG CTTCAGCAAG TACCAGTGCT TCAGCTTCAG CATCAACCAG      1740
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1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCTC   1800

AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGCGCC TCAGCCTCAG CATCAACGAG   1860

TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC   1920

AGCGTCAACC AGTGCTTCAG CCTCAGCATC AACAAGTGCG TCAGCCTCAG CAAGTATCTC   1980

AGCGTCTGAA TCGGCATCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC   2040

AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGTGCG TCAGCCTCAG CATCGACAAG   2100

CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC   2160

AACCAGTGCA TCTGAATCGG CATCAACCAG TGCGTCAGCC TCAGCAAGTA CTAGTGCATC   2220

GGCTTCAGCA TCAACCAGTG CCTCGGCTTC AGCGTCAACC AGTGCGTCAG CTTCAGCAAG   2280

TACCAGTGCT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC   2340

GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTCGACA AGCGCCTCAG CTTCAGCAAG   2400

TACCAGTGCG TCAGCCTCAG CGTCGACAAG TGCGTCAGCT ACAGCAAGTA CTAGTGCATC   2460

AGCTTCAGCA TCAACGAGTG CATCGGCTTC GGCGTCAACC AGTGCATCAG AGTCAGCAAG   2520

TACCAGTGCG TCAGTTCACG CATCAACAAG   2550

(2) INFORMATION FOR SEQ ID NO: 365:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1436 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TGCGTCGGCT TCAGCATCAA   60

CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAC   120

CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC   180

CAGCGCCTCA GCTTCAGCAA GCACCAGTGC GTCAsCTCAG CAAGTACCAG CGCCTCAGCC   240

TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA   300

AGTGCGTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT   360

TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG   420

AGTGCGTCCG CTTCAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT   480

TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA   540

TCAGCTTCTG AATCTGCATC AACCAGTGCG TCAGCCTCAG CATCGACAAG CGCCTCAGCT   600

1381

TCAGCAAGTA	CCAGTGCGTC	AgCCTCAGCA	AGTACCAGTG	CTTCAGCCTC	AGCGTCGACA	660
AGTGCGTCGG	CCTCAACCAG	TGCATCTGAA	TCGGCATCAA	CCAGTGCGTC	AGCCTCAGCA	720
AGTACTAGCG	CCTCAGCCTC	AGCATCAACG	AGTGCGTCCG	CTTCAGCAAG	TACTAGTGCA	780
TCAGCTTCAG	CAAGTACTAG	CGCCTCAGCC	TCAGCGTCGA	CAAGCGCCTC	AGCTTCAGCA	840
AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	AGTGCGTCGG	CTTCAGCAAG	TACCTCAGCG	900
TCTGAATCAG	CATCAACAAG	TGCGTCGGCT	TCAGCATCAA	CGAGTGCATC	AGCTTCAGCA	960
TCAACAAGTG	CTTCAGCTTC	AGCAAGTACC	AGTGCGTCGG	CTTCAGCATC	AACGAGTGCT	1020
TCAGTCTCAG	CGTCAACCAG	TGCCTCTGAA	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	1080
AGCACCAGTG	CTTCGGCTTC	AGCGTCAACG	AGTGCGTCTG	AGTCAGCATC	AACGAGTGCG	1140
TCAGCCTCAG	CAAGCACATC	AGCTTCTGAA	TCTGCATCAA	CCAGTGCGTC	AGCTTCCGCA	1200
TCAACAAGCG	CCTCGGCCTC	AGCAAGTACA	AGTGCTTCAG	CCTCAGCATC	AACCAGTGCA	1260
TCAGCTTCAG	CCTCAACAAG	TGCTTCAGCC	TCAGCGTCAA	CCAGTGCCTC	GGCTTCAGCA	1320
AGTACCAGTG	CGTCAGCTTC	AGCAAGCACA	AGTGCGTCAG	CTTCAGCATC	AACCAGTGCT	1380
TCGGCTTCGG	CATCAACAAG	TGCCTCAGCA	TCAGCATCAA	CGAGTGCGTC	AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 735 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA	CACCGTGCTG	ACCAGCACCC	GTTCCTGCGA	TAATTTTCTT	TTTACCCATG	60
CGTwTGGCAA	GCCAAACTTG	TCCTAAGGCA	TTGTTAATCT	TGTGGGCTCC	TGTATGGTTA	120
AGGTCTTCCC	GTTTGAGATA	AATCTTGCTC	CGCCAATATG	CTGGGTCAAG	TTTTTTGCGT	180
AATAAAGAGG	AGTTTCACGT	CCTACGTACT	GGCGCAAAAG	CTGGTTTAAT	TCCTCTTGGA	240
AACTTGGGTC	TGCCTGACTT	TCACGGTAGG	CCTTCTCCAA	CTCCAAAACT	GCTGTCATCA	300
ATGTTTCTGG	GACAAAACGT	CCGCCGAATT	TTCCGTAAAA	TCCATCTTTA	TTTGGTTCCT	360
GATATGCCAT	GCTTTACCCT	CTCTATAAAT	CTTCTAATCT	TTTCATGATC	TTTTTGTCCA	420
TCTGTCTCCA	CTCCGCTCGA	TACATCTACT	GCATAGGGAG	TAAAGTGTTG	AATTGCTTTT	480
ACTACATTAT	CTTCATTAAG	GCCACCTGCG	ATAAAGAAGG	GCTGTGCTAG	TCCAGTCGTA	540

1382

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TCCAGTTGAC CCCAATCAAA GGGCTGGCCA CTTCCTGCCA CAGGGGCATC AAAGAGTAGA      600

TAATCTGCCT GAGAATTGGG GACATGCCCA TTTCCATCTA CCTGCACAGC CTGAATACTG      660

GCACAAGGCA AATTCTCAAA TAAATCATCT GCCACCTGAC CGTGAACTTG AACCAAGTCC      720

AAGCCGGGGA TCCTC      735
```

(2) INFORMATION FOR SEQ ID NO: 367:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1702 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

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TACTAGCGCC TCAGCCTCAG CGTCAACAAG TGCATCGGCT TCAGCATCAA CGAGTGCGTC       60

CGCTTCAGCA AGTACTAGCG CCTCAGCCTC AGCGTCAACA AGTGCATCGG CTTCAGCGTC      120

AACGAGTGCG TCTGAGTCAG CATCAACGAG TGCGTCAGCC TCAGCAAGCA CATCAGCTTC      180

TGAATCTGCA TCAACCAGTG CGTCAGCCTC AGCATCGACA AGCGCCTCAG CTTCAGCAAG      240

TACCAGTGCG TCAGCCTCAG CGTCGACAAG TGCGTCGGCT TCAGCAAGTA CCAGTGCGTC      300

AGCCTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCGTCGG CCTCAACCAG      360

TGCATCTGAA TCGGCATCAA CCAGTGCGTC AGCCTCAGCA AGTACTAGTG CATCAGCTTC      420

AGCATCAACG AGTGCATCGG CTTCAGCATC AACCAGTGCA TCAGAGTCAG CAAGTACCAG      480

TGCGTCAgCT TCCGCATCAA CAAGTGCCTC GGCTTCAGCA AGTACTAGCG CCTCAGCCTC      540

AGCGTCAACA AGTGCTTCAG CTTCCGCGTC AACCAGCGCC TCGGCCTCAG CAAGTATCTC      600

AGCGTCTGAA TCGGCATCAA CAAGTGCCTC GGCTTCAGCA TCAACGAGTG CATCAGTCTC      660

AGCAAGCACC AGTGCGTCGG CCTCAGCAAG CACCAGCGCG TCTGAATCCG CATCAACCAG      720

TGCCTCAGCT TCAGCAAGTA CCTCAGCATC TGAATCAGCA TCAACAAGTG CATCGGCTTC      780

AGCAAGCACA AGTGCTTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG      840

TGCGTCCGCT TCAGCAAGTA CTAGCGCCTC AGCATCAGCG TCAACAAGTG CTTCGGCTTC      900

AGCGTCAACG AGTGCGTCTG AGTCAGCATC AACGAGTACG TCAGCCTCAG CAAGCACATC      960

AGCTTCTGAA TCTGCATCAA CCAGTGCGTC AGCCTCAGCA TCGACAAGCG CCTCAGCTTC     1020

AGCAAGTACC AGTGCGTCAG CCTCAGCAAG TACCAGTGCT TCAGCCTCAG CGTCGACAAG     1080

TGCGTCGGCC TCAACCAGTG CATCTGAATC GGCATCAACC AGTGCGTCAG CCTCAGCAAG     1140

TACTAGCGCC TCAGCCTCAG CATCAACGAG TGCGTCCGCT TCAGCAAGTA CTAGTGCATC     1200
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1383

AGCATCAGCA	TCAACGAGTG	CATCGGCTTC	AGCAAGTACC	AGCGCCTCAG	CTTCAGCAAG	1260
CACCAGTGCG	TCAGCCTCAG	CAAGTACCAG	CGCCTCAGCC	TCAGCAAGCA	CCAGTGCCTC	1320
AGCTTCAGCA	AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	AGTGCGTCGG	CTTCAGCAAG	1380
TACCTCAGCG	TCTGAATCAG	CATCAACGAG	TGCATCAGCT	TCAGCATCAA	CAAGTGCTTC	1440
AGCTTCAGCA	AGTACCAGTG	CGTCGGCTTC	AGCATCAACG	AGTGCTTCAG	TCTCAGCGTC	1500
AACCAGTGCC	TCTGAATCAG	CATCAACAAG	TGCCTCGGCT	TCAGCAAGCA	CCAGTGCGTC	1560
GGCTTCAGCA	AGTACTAGTG	CATCGGCTTC	AGCATCGACA	AGTGCGTCTG	AATCGGCATC	1620
AACGAGTGCT	TCGGCTTCAG	CATCAACGAG	TGCGTCAGCC	TCAGCAAGCA	CATCAGCTTC	1680
TGAATCTGCA	TCAACCAGTG	CG				1702

(2) INFORMATION FOR SEQ ID NO: 368:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 941 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCAT	CAGCTTCAGC	CTCAACAAGT	GCTTCAGCCT	CAGCGTCAAC	CAGTGCCTCG	60
GCTTCAGCAA	GTACCAGTGC	GTCACTTCAG	CAAGCACAAG	TGCGTCACTT	CAGCATCAAC	120
CAGTGCTTCG	GCTTCGGCAT	CAACAAGTGC	CTCAGCATCA	GCATCAACGA	GTGCGTCACC	180
TCAGCAAGTA	CTAGTGCATC	AGCATCAGCA	TCAACCAGTG	CATCAGCCTC	AGCAAGTATC	240
TCAGCGTCTG	AATCGGCATC	AACGAGTGCA	TCAGCATCAG	CATCAACGAG	TGCATCGGCT	300
TCAGCGTCAA	CCAGTGCATC	AGTCTCAGCA	AGCACCAGTG	CGTCGGCTTC	AGCATCAACG	360
AGTGCCTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGCGTCAGCC	420
TCAGCAAGTA	CTAGTGCATC	GGCTTCAGCA	AGCACCAGTG	CGTCGGCTTC	AGCATCAACC	480
AGTGCCTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGCGTCAGCC	540
TCAGCAAGTA	CTAGTGCATC	AGCATCAGCA	TCAACGAGTG	CATCGGCTTC	AGCAAGTACC	600
AGCGCCTCAG	CTTCAGCAAG	CACCAGTGCG	TCAGCCTCAG	CAAGTACCAG	CGCCTCAGCC	660
TCAGCAAGCA	CCAGTGCCTC	AGCTTCAGCA	AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	720
AGTGCGTCGG	CTTCAGCAAG	TACCTCAGCG	TCTGAATCAG	CATCAACGAG	TGCATCAGCT	780
TCAGCATCAA	CAAGTGCTTC	AGCTTCAGCA	AGTACCAGTG	CGTCGGCTTC	AGCATCAACG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT   900

TCAGCAAGCA CCAGTGCGTC GGCTTCAGCA AGTACTAGTG C   941

(2) INFORMATION FOR SEQ ID NO: 369:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 869 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA   60

GTGCATCAGA GTCAGCAAGT ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT   120

CAGCAAGCAC CAGTGCGTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA   180

GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT   240

CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA   300

GTGCGTCTGA ATCGGCATCA ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT   360

CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA   420

GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT   480

CAGCATCAAC GAGTGCGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA   540

GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCGTCAGCCT   600

CAGCGTCGAC AAGTGCGTCG GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA   660

GTGCGTCAGC CTCAGCGTCG ACAAGTGCGT CGGCCTCAAC CAGTGCATCT GAATCGGCAT   720

CAACCAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT   780

CGGCTTCAGC ATCAACCAGT GCATCAGAGT CAGCAAGTAC CAGTGCGTCA GnTTCCGCAT   840

GCAACAAGTG CCTCGGCTTC AGCAAGTAC   869

(2) INFORMATION FOR SEQ ID NO: 370:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 750 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA   60

1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA   120

TCAACGAGTG CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAGTGCA   180

TCAGTCTCAG CAAGCACCAG TGCGTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA   240

AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA   300

TCGGCTTCAG CAAGCACCAG TGCGTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA   360

AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA   420

TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA   480

AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC   540

TCAGCTTCAG CAAGTACCAG TGCGTCAGCC TCAGCGTCGA CAAGTGCGTC GGCTTCAGCA   600

AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAGTGCT   660

TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCGTC CGCTTCAGCA   720

AGTACTAGCG CCTCAGCATC AGCGTCAACG   750

(2) INFORMATION FOR SEQ ID NO: 371:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 957 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGGAAAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC   60

GGAAATGGCT AAGATGCGCG TGTTAGAACT TGATTTGATG AATGTCGTTG CAGGGACACG   120

CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG   180

CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCTGGTA GCGGGATTGA   240

TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGAA CTTTGAGAAC   300

GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC   360

TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT   420

ACAAGGTTTG AAGGCGACTT ATGAGAAACA TCACCGTGTA CAAATCACAG ATGAAGCGGT   480

TGAAACAGCG GTTAAGATGG CTCATCGTTA TTTAACCAGT CGTCACTTGC CAGACTCTGC   540

TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAAT AAGGCAAAGC ATGTAAAAGC   600

AGACGATTCA GATTTGAGTC CAGCTGACAA GGCCCTGATG GATGGCAAGT GGAAACAGGC   660

1386

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AGCCCAGCTA ATCGCAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC     720

TGATATTTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGACTCAAAC     780

GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA     840

TCAAGCTGTT TCAAGCATTA GCCGTGCCAT TCGCCGCAAC CAGTCAGGGA TTCGCAGTCA     900

TAAGCGTCCG ATTGGTTCCT TTATGTTCCT AGGGCCTACA GGTGTCGGGG TATCCGA       957
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(2) INFORMATION FOR SEQ ID NO: 372:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 807 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

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CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG      60

GCTTCAGCGT CAACCAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA     120

ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT     180

GAATCAGCGT CAACCAGTGC TTCGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA     240

ACCAGCGCCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG     300

GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA     360

ACGAGTGCTT CGGCTTCAGC AAGCACAAGC GCCTCGGGTT CAGCATCAAC GAGTACGTCA     420

GCTTCAGCGT CAACCAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAAGT     480

ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA     540

GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG     600

ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCTTCAGCCT CAGCGTCGAC AAGTGCGTCG     660

GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGCGT CAGCCTCAGC AAGTACTAGT     720

GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAGTGC GTCAGCTTCA     780

GCAAGTACCA TGTGCTTCAT GTCTCAG                                        807
```

(2) INFORMATION FOR SEQ ID NO: 373:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1068 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGCGTCCG CTTCAGCAAG TACTACCGCC TCAGCCTCAG   60

CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTG   120

CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CACCTCAGCA   180

TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGCGTCAC CTCAGCGTCG ACAAGTGCGT   240

CGGCTTCAGC AAGTACCAGT GCGTCAsCTC AGCAAGTACC AGTGCGTCAC CTCAGCGTCG   300

ACAAGTGCGT CGGCCTCAAC CAGTGCATCT GAATCGGCAT CAACCAGTGC GTCACCTCAG   360

CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAGTG   420

CATCAGAGTC AGCAAGTACC AGTGCGTCAG cTTCCGCATC AACAAGTGCC TCGGCTTCAG   480

CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCTTC AGCTTCCGCG TCAACCAGCG   540

CCTCGGCCTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAGTGCC TCGGCTTCAG   600

CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGCGTC GGCCTCAGCA AGCACCAGCG   660

CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTCAGCAAG TACCTCAGCA TCTGAATCAG   720

CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCTTC AGCCTCAGCA AGTATCTCAG   780

CGTCTGAATC GGCATCAACG AGTGCGTCCG CTTCAGCAAG TACTAGCGCC TCAGCATCAG   840

CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA   900

CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAGTGCG TCAGCCTCAG   960

CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCGTC AGCCTCAGCA AGTACCAGTG   1020

CTTCAGCCTC AGCGTCGACA AGTGCGTCGG GCTCAACCAG TGCATCTG   1068

(2) INFORMATION FOR SEQ ID NO: 374:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 620 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGCGT CAACCAGTGC CTCTGAATCA GCTTCAACAA   60

GTGCCTCGGC TTCAGCAAGC CCCAGTGCGT CGGCTTCAGC AAGTACTAGT GCATCGGCTT   120

CAGCATCGAC AAGTGCGTCT GAATCGGCAT CAACGAGTGC TTCGGCTTCA GCATCAACGA   180

GTGCGTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATcAACCAGT GCGTCCGyTT   240

1388

```
CAGCGTCAAC CAGTGCGTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA        300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCCGCCTCA ACCAGTGCGT        360
CGGCTTCAGC AAGCACAAGT GCGTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT        420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT        480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA GCTTCAGCAA        540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAACCAGT GCATCTGAAT        600
CGGCATCAAC CAGTGCGTCA                                                    620
```

(2) INFORMATION FOR SEQ ID NO: 375:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 720 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```
GTATTGGGGC GCCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA         60
AACCATTTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGCCCA AGAAAGCCAA        120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT        180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TTAACGGCCA        240
AGTGGTGCGT GAACTAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA        300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTTC        360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTTGTCGAC CTCTTGCCCA ATGTCAAAGA        420
GCGTATTTAC CCTGTGGGTC GTTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA        480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT        540
CGCGCGTGTT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA        600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGGTTTT GTAGCCTCTA CACCATAAAT        660
ATTTGCTAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT        720
```

(2) INFORMATION FOR SEQ ID NO: 376:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 648 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```
CGCCATTTCC CATCGTACCG CCGAAAATCC CAGCGCCTCA GCCATCAAAT ATCCTATCAA          60

CGTTCTCAAA AAAAGTGACC GCTCTCTCAT CATGTTTCCA AGTGGTAGCC GCCACTCAAA         120

CGATGTCAAG GGGGGCGCAC ACTskATTGC CAAAATGGCC AAGGTCCGTA TCATGCCGGT         180

TACCTACACC GGTCCCATGA CTTTGAAGGG CTTGATTAGC CGTGAACGTG TCGATATGAA         240

CTTTGGAAAT CCAATCGATA TCTCAGATAT CAAGAAAATG AATGATGAAG GCATTGAAAC         300

AGTCGCCAAT CGTATTCAAA CAGAATTCCA ACGTCTGGAC GAAGAAACGA AACAATGGCA         360

CAATGATAAA AAACCAAATC CACTCTGGTG GTTTATCCGC ATCCCTGCCC TCATCCTTGC         420

TATTATCCTC GCTATCCTAA CCATCATCTT TAGCTTTATC GCAAGCTTCA TCTGGAACCC         480

AGATAAGAAA AGAGAAGAAC TTGCATAGAA GAAATGAACC TTGGCCAAAC AGCTAAGGTT         540

TTCATTTATA TAGTAGATTG GwACTAGAAT AGTACACCTC.TACTTCTAAA ACATTTTTAG         600

AAATCGATTT GACTGTCCTG ATCGATTTGT CCTAATCTTA TTTCAATT                      648
```

(2) INFORMATION FOR SEQ ID NO: 377:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 690 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

```
GTGCATCGCT TTCAGCATCG ACAAGTGCGT CTGAATCGGC ATCAACGAGT GCTTCGGCTT          60

CAGCATCAAC GAGTGCGTCA GCTTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA         120

GTGCGTCCGC TTCAGCGTCA ACCAGTGCGT CGGCTTCAGC GTCGACAAGT GCTTCGGCTT         180

CAGCATCAAC GAGTGCGTCG GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT         240

CAACCAGTGC GTCCGCTTCA GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT         300

CTGAATCGGC ATCAACGAGT GCGTCGGCCT CAGCAAGCGC AAGTACCTCA GCGTCAGCTT         360

CCGCCTCAAC CAGTGCGTCG GCTTCAGCAA GCACAAGTGC GTCAGCCTCA GCAAGTATCT         420

CAGCGTCTGA ATCGGCATCA ACGAGTGCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT         480

CAGCAAGCAC ATCAGCTTCT GAATCGGCAT CAACCAGTGC GTCAGCCTCA GCATCGACAA         540

GCGCCTCAGC TTCAGCAAGT ACCAGTGCTT CAGCCTCAGC GTCGACAAGT GCGTCGGCCT         600

CAACCAGTGC ATCTGAATCG GCATCAACCA GTGCGTCAGC CTCAGCAAGT ACTAGTGCAT         660
```

                                    1390
CAGCTTCAGC ATCAACGAGT GCATCGGCTT   690

(2) INFORMATION FOR SEQ ID NO: 378:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1003 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
        .   (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTC CAATATGTGC ACGTTGGAAT GTTAGTGCTT   60

ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT   120

CTTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT   180

TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTTATA TACTAGTGGT GTTTTTGGGG   240

CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTTATACT TACAGTTGTT CTGCTCCAAA   300

GAGCTTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAAATG   360

CACAGGATAA CCTGATGCAT TTTTTTAGCG ACAATGCTTG CTACTTCCTT CTGTCGAATT   420

TAGACAATTT TAAACCCCAA TTATTCACCC CAAATCTAAA AACCATCCAG AATCCTTGCC   480

TTAGCTTAGA TCCTGGATGG TTTCTTTTTT CACCCAATGG GTGTTTTTTA CTAGACAAAA   540

AAGAGTTTCC CCTTTATGGT ATAAGTGTAG AAAAAAACAC AAAAAGAAAG GAAACTCACA   600

TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCTTT TTACCAACTA TCTTTCGATG   660

GAGGTCATTT AACCCAGTAT GGTGGTCTTA TCTTTTTTCA GGAACTTTTT TCCCAGTTGA   720

AACTAAAAGA GCGGATTTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT   780

ATTCGGATTC AGATATCCTT GTCCAGTTCC TCTTTCAACT GTTAACAGGT TATGGAACGG   840

ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTTCC AAAATTATTG GAAGGAGGGC   900

AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTTCCAG AACTGACGAG GAAACAGTCC   960

ATAGTTTGCG ATGCCTCAAC CTTGAATTGG TCGAATTCTT TTT   1003

(2) INFORMATION FOR SEQ ID NO: 379:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 738 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

```
CCGATGATTC TGATTGGTTT GCTCTTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT        60

TGAAATACTA ATTGTTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT       120

ACAACCCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG       180

CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT       240

TATTCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACTT CAGATATTCA       300

CCTTTTGTGG ATTGGTCTGA AGTTTTCTTT TTTATACTCA ATGAAAATCA AAGAGCAAAC       360

TAGGAAGCTA GCCGCAckGC TCAAAACACC GTTTTGAGGT TGTAGATATA ACTGACGAGc       420

GACTCAAAAC ACCGTTTTGA GGTTGTAGAT ATAACTGACG AGcGACTCAA AACACCGTTT       480

TGAGGTTGTG GATAGAACTG ACGAGcGACT CAAAACACCG TTTTGAGGTT GTGGATAGAA       540

CTGACGAAGT CGcTCAAAAC ACCGTTTTGA GGTTGTGGAT AGAACTGACG AAtgctCAAA       600

ACACCGTTTT GAGGTTGTGG ATAGAACTGA CGAAGCgaaC ATATATACAG CAAGGCGACG       660

CTGACGTGGT TTGAAGAGTA TTACTGTCTA TATTTTTGGT AAAAATCAAC TTTTACTTGG       720

ATGAAGGTTT TTTTTTT                                                       738
```

(2) INFORMATION FOR SEQ ID NO: 380:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 695 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```
CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC        60

GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAACCAGC AATAATTTCT TTGGCACGGT       120

TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTCC TTCTTCGTCT ATATCAATCT       180

TAACACCTGT TTCAGCGATA ATCTTGTCGA TGGTTTCTCC ACCCTTACCG ATGACAATCT       240

TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTTCGG AGCAGTTGGA GCCAATTCTG       300

GACGAACTTC TGGAATGGTT GCTTCAATGA CATCAAGGAT TTCAAAACGC GCTTTCTTGG       360

CTTGAGCAAG AGCCTCCGTC AAGATTTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT       420

GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT       480

CTTCCAAACC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA       540

TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC       600
```

1392

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTC CAAAACTTCT GCTACTAGAC   660

GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG   695

(2) INFORMATION FOR SEQ ID NO: 381:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 691 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT   60

TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT   120

CAGAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC   180

CAGAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTTCTTT TTTCACCCAA TGGGTGTTTT   240

TTACTAGACA AAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAAA CACAAAAGA   300

AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTTACCAA   360

CTATCTTTCG ATGGAGGTCA TTTAACCCAG TATGGTGGTC TTATCTTTTT TCAGGAACTT   420

TTTTCCCAGT TGAAACTAAA AGAGCGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC   480

CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTTCA ACTGTTAACA   540

GGTTATGGAA CGGACTATGC TTGTAAAGAA TTGTCAGCTG ATGCCTACTT TCCAAAATTG   600

TTGGAAGGAG GGCAGCTTGc TTCACAGCCA ACCTTATCCC GwTTTCTTTC CAGAACTGAC   660

GAGGAAACAG TCCATAGTTT GCGATGCCTC A   691

(2) INFORMATION FOR SEQ ID NO: 382:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 750 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC   60

CAAGTTATGC CTAAAGGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT   120

CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCCGACT   180

AATATTGGCT TTGCATTTAT TCCTCCATAC ACACCAGAGA TGAACCCCAT TGAACAAGTG   240

1393

```
TGGAAAGAGA TTCGTAAACG TGGATTTAAG AATAAAGCCT TTCGAACTTT GGAAGATGTC        300

ATACAAGGAC TGGAGAAGGA GGTGATAAAG TCCATCGTTA ATCGGAGACG GACTAGAATG        360

CTTTTTGAAA ACAGATGAGT ATAAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT        420

CTGATGAATT TATAGTAAAA TGAAATAAGA ACAGGATAGT CAAATCGATT TCTAACAATG        480

TTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTTGGGG AGTGATAGAA        540

AAGCCCTTCA TCAGCCAATC TACTTGTTCA GGTGCGAGAG CTTTGACATC CTTTTCTGTA        600

CTGGACCAAG TCAGTTTTCC GTTCTCAAAG CGTTTATATA ATATCCAAAA TCCTTGACCA        660

TCCCAGTAAA GAACTTTAAA GCGGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG        720

GAGAAAGGAT CCAATTCAAA GTGGGTTTGG                                          750
```

(2) INFORMATION FOR SEQ ID NO: 383:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 738 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```
TCAAATTCTT CGTGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTTCACT        60

ACTCGAGTCG CAGCTTCACG GGCCAATTTC TCTTCTACTT GAACTGCCTT TTGGAGGTCA        120

CTGTTGTAGG CTGCAATGAT TTCAGCTTGC AATTCAGCAT CCACGTGAAG CAATTCCACT        180

TCTGCTTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATTCTTTG        240

ACAGCTTCGT GCCCTTTAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTTGGCA        300

CCAGACTCTA CCATGTTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT        360

TGCTCTGCTT GTTCTTGACT TGGGTTGATG ATGATTTGGC CATCTACATA TCCCACTTGT        420

ACCCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA        480

AACATAGCAG CCATTGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT        540

TGGACTTCAT TACGGAAACC TTCCGCAAAC ATAGGACGAA TCGGACGGTC AATCAAACGC        600

GCTGTCAAGG TCGCATCTGT TGAAGGACGT CCTTCACGTT TCATAAAGCC ACCAGGAAAC        660

TTCCCAGCCG CATACATTTT TTCTTCGTAG TTGACTTGGA GTGGGAAGAA ATCCTCAGTT        720

GCCATTTTCT GGGGATCC                                                      738
```

(2) INFORMATION FOR SEQ ID NO: 384:

1394

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 657 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT   60

TAGGAACTAT ATATGAGTTC TCTAGTCTGG AGATTTTTCA ATAGACTTCG TTATTGGGCG   120

GTTACTTTCG AAACTTTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATTCTTTT   180

GGGGTCAAAC TCAGTAACTT ATTCGCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC   240

AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATTATCTG AATCATCTCC TTCTTGTTCT   300

CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT   360

TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAAC CTTATCAAAT TCATCACTTT   420

TCGCAGAAAC CATCATAATT GGAGTTTTGA CGCCTTTGGC TCTCAGCCGC TTACAAACTT   480

CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTTCTGTTT   540

CTGCCAAAGC TAAGGCCTTC CGTCCATTTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC   600

TTAAATGGTA GTCAAGCAAT TTCAGAATGT GTTCTTCATC ATCCACTAAT AAGACTT   657

(2) INFORMATION FOR SEQ ID NO: 385:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 586 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG   60

CACCAGTGCG TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGTA TCTCAGCGTC   120

TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC   180

ACCAGTGCGT CGGCTTCAGC ATCAACCAGT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT   240

GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCATCAGCA TCAGCATCAA   300

CGAGTGCATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGCGTCAC   360

CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC   420

CAGTGCGTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA   480

1395

TCAGCATCAA CGAGTGCGTC AGCTTCAGCA TCAACCAGTG CCTCAGCCTC AGCAAGTATC   540

AGTGCGTCAG CTTCAGCATC AACGAGTGCG TCAGCTGCAG CAAGTA   586

(2) INFORMATION FOR SEQ ID NO: 386:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 451 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAGTGCT TCAGCTTCAG   60

CAAGTACCAG TGCGTCGGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAGTG   120

CCTCTGAATC CGCATCAACA AGTGCCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG   180

CGTCAACGAG TGCGTCTGAG TCAGCATCAA CGAGTGCGTC ACCTCAGCAA GCACATCAGC   240

TTCTGAATCT GCATCAACCA GTGCGTCAGC TTCCGCATCA ACAAGCGCCT CGGCCTCAGC   300

AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC   360

TTCAGCCTCA GCGTCAACCA GTGCCTCGGC TTCAGCAAGT ACCAGTGCGT CAGTTcAGCA   420

AGCACAAGTG CGTCAATTTA GCATCAACCA G   451

(2) INFORMATION FOR SEQ ID NO: 387:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 425 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAG CGCGTTTGAA TCCGCATCAA   60

CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC   120

GGCTTCAGCA AGCACAAGTG CTTCAGCtCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA   180

ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG   240

GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC   300

ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA   360

GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTCG   420

1396
ACAAG   425

(2) INFORMATION FOR SEQ ID NO: 388:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 572 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTC ATCATGTAGT   60

AGACAAACTC TTCATACTCC AACACTTGCC CATTTTATGC GAATCTCATC TATTTTTTCT   120

TTTTTTTGCA ATTTAGCTGA TTTTTCTTTT TTACCATTTA CAGTCACGCG CCCAGCCTTG   180

AGCAAGTTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT   240

CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTCG   300

TTTCATACTC TTCAAAAATC TCTTCAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT   360

ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTCGTCAGT   420

TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC kAGTkTGCTC   480

TTTGATTTwC ATTGAGTATC AGATTTAGGA AATTAACTTC CTCGkCTCCA AAAAAkAGCT   540

AAAACAATCA AGGCTCCTAA AATCGCTGGG AT   ·   572

(2) INFORMATION FOR SEQ ID NO: 389:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 505 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT   60

CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT   120

CAAcAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT   180

CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGCGTCA GCCTCAGCAT   240

CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT   300

CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAGTGC ATCTGAATCG GCATCAACCA   360

GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT   420

1397

CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA   480

GCGCCTCAGC TTCAGCAAGC ACCGG   505

(2) INFORMATION FOR SEQ ID NO: 390:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 447 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC   60

AATACTGTAC TTTTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT   120

AAACTTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTTAC TAAGTATTAT CTAGGAAATA   180

GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAAA   240

ATTTAAGTCA AAAAAATTAA CATTAGTTAA TTTATTTTTT AGCACACATT AAAAAATAAG   300

ATTAGTACTC AATGAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGAT TGCTCAAAAC   360

AGTGTTTTGA GGTTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT   420

GGATAGAACT GACGAAGTCG GTACCGA   447

(2) INFORMATION FOR SEQ ID NO: 391:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 572 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAAT GTTGTAATAT TTTATTGAAT AAGATAGGCC   60

TTGATATTAA GCACTTTGGG ACGTTCTCCC TTAGTGCTTT TTTGATTTCT CTTAGTATCC   120

AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAAATGAA   180

CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTAA   240

AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTTCCA   300

AATCTCACGT AATACCATTT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA   360

CCACCAAGTA TAGTGTATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT   420

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                                        1398
AAATTAATTT GACTTTCCTG ATAGAGATGT TCACATCTTA TTTCAAACTA CTATATAAGT        480

TCTATAATCT CTTTATAAGA TTTGCCCATC AGACAAAATA GAACGATTTG AAGGCGTTTA        540

TGATATTTAG CTGTACGAGA GTCTTTTAAA AG                                      572
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MISSING UPON TIME OF PUBLICATION

1400

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

1402

What Is Claimed Is:

1.   Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.

2.   Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.

3.   The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

4.   The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:

a)   a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;

b)   search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

c)   retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

7. A method for identifying an expression modulating fragment of *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a degenerate variant thereof.

9. A vector comprising any one of the fragments of the *Streptococcus pneumoniae* genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.

10. An isolated fragment of the *Streptococcus pneumoniae* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a degenerate variant thereof.

11. A vector comprising any one of the fragments of the *Streptococcus pneumoniae* genome of claim 8.

12. An organism which has been altered to contain any one of the fragments of the *Streptococcus pneumoniae* genome of claim 8.

13. An organism which has been altered to contain any one of the fragments of the *Streptococcus pneumoniae* genome of claim 10.

1404

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;

b) identifying members of said library which contain sequences that hybridize to said target sequence; and

c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

a) isolating mRNA, DNA, or cDNA produced from an organism;

b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;

c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

1405

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

130

20. A method for producing a polypeptide in a host cell comprising the steps of:

a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus*

135   *pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and
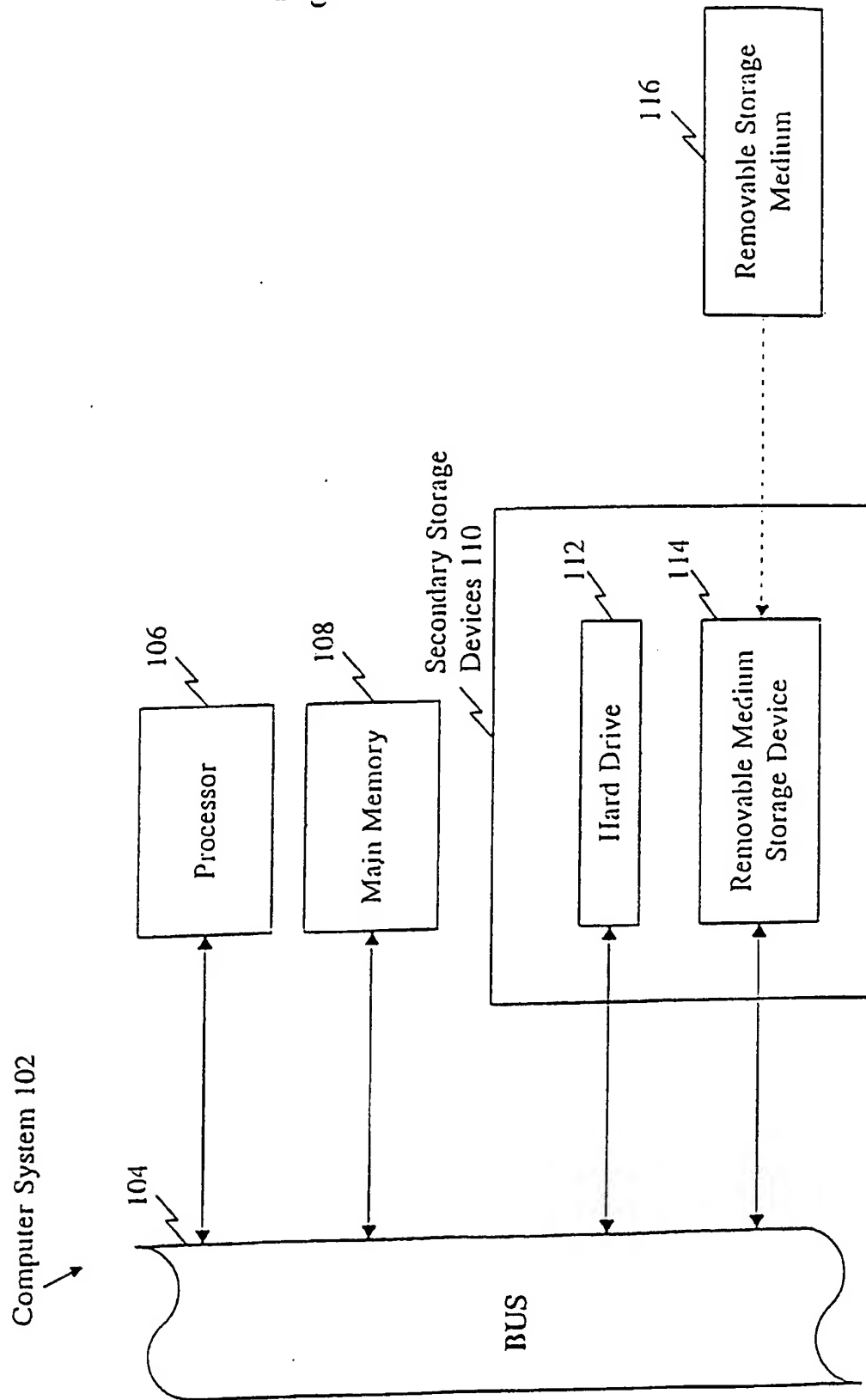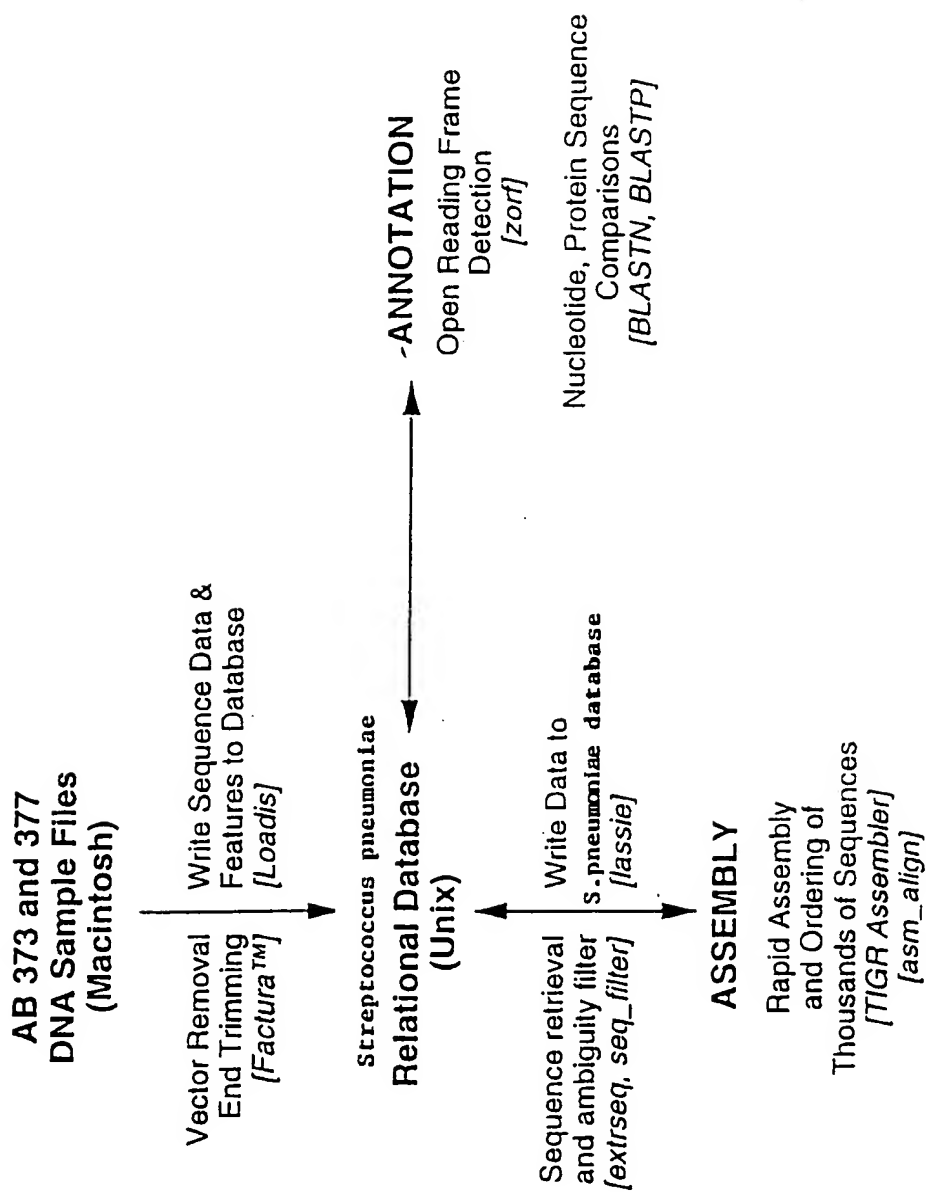
b) isolating said protein.

Figure 1

Figure 2